



CC immunogens to produce antibodies that selectively bind to integrin I-  
CC domain; and for identifying a modulator of integrin activity, or of  
CC interaction of an integrin and a cognate ligand. The polypeptide of the  
CC invention, or antibodies (preferably anti- $\alpha$ -1 antibody) is useful for  
CC treating or preventing an integrin mediated disorder which is an  
CC inflammatory or autoimmune disorder in a subject and for inhibiting the  
CC binding of an integrin to a cognate ligand in a subject. A therapeutic  
CC composition comprising the peptide of the invention is useful for  
CC creating an integrin mediated disorder such as Crohn's disease, nephritis  
CC ; human immunodeficiency virus (HIV), myocardial infarction, Sjogren's  
CC syndrome, rheumatoid arthritis, dermatitis. The polypeptides and/or  
CC active or antigenic fragments are useful as reagents for diagnosis of  
CC integrin-mediated disorders. The present sequence represents the human  
CC polypeptides of the invention  
XX  
SQ Sequence 1170 AA;  
Query Match 100.0%; Score 6106; DB 5; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKDSCTTMMAMALLSGFFFPAPASSYNLDVVGARSFSPRRGRFRVYLVQVNGVYGA 60  
DB 1 MKDSCTTMMAMALLSGFFFPAPASSYNLDVVGARSFSPRRGRFRVYLVQVNGVYGA 60  
QY PGEENSTSLYQCCSGTGCHLPVTLRGSNYSKYLGMATLDPDGSILACDPGLSRTCD 120  
DB PGEENSTSLYQCCSGTGCHLPVTLRGSNYSKYLGMATLDPDGSILACDPGLSRTCD 120  
QY 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVDLFLPDGSMSLQPDFQKILDFMK 180  
DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVDLFLPDGSMSLQPDFQKILDFMK 180  
QY 181 DVMKTLSTSYQPAANVPSTSYKTRPDSYVKKRDPALLKHYKAMLLNTNGALNV 240  
DB 181 DVMKTLSTSYQPAANVPSTSYKTRPDSYVKKRDPALLKHYKAMLLNTNGALNV 240  
QY 241 ATEVFREBELGARPRATKVLIIITDGEATDSGNIDAAKIIIRYIIGIGHPOTKXSOETLH 300  
DB 241 ATEVFREBELGARPRATKVLIIITDGEATDSGNIDAAKIIIRYIIGIGHPOTKXSOETLH 300  
QY 301 KFAKSPASEFVKIILDFEKLKDLFTELQKIIYIEGTSKODLTSFNNELSSSGISADLSR 360  
DB 301 KFAKSPASEFVKIILDFEKLKDLFTELQKIIYIEGTSKODLTSFNNELSSSGISADLSR 360  
QY 361 GHAVVGAAGADWAGGFLDLKADLQDDTFIGNEPITPEVRAGYLGYYTWM.PSRQKTSLL 420  
DB 361 GHAVVGAAGADWAGGFLDLKADLQDDTFIGNEPITPEVRAGYLGYYTWM.PSRQKTSLL 420  
QY 421 ASGARPRYOHMGRVLLFOEPQGGHMSQVQTIHGTOIGSFPGGBLGGVVDODGETELLII 480  
DB 421 ASGARPRYOHMGRVLLFOEPQGGHMSQVQTIHGTOIGSFPGGBLGGVVDODGETELLII 480  
QY 481 GAPPFYGEORGRVFIYQRRQLGFEVEVELQGDPRYPLGRGGEAITALTDINGGLVDVA 540  
DB 481 GAPPFYGEORGRVFIYQRRQLGFEVEVELQGDPRYPLGRGGEAITALTDINGGLVDVA 540  
QY 541 VGAPLEBEGGAVYINRGHGGISPOPSQRIEQTQVLSGICQMGKRSIHGYKLEGGGLADVA 600  
DB 541 VGAPLEBEGGAVYINRGHGGISPOPSQRIEQTQVLSGICQMGKRSIHGYKLEGGGLADVA 600  
QY 601 VGASOMTVLSRPVMDVTLMSFSPARIPVHEVCSTSNKMKKEGNITICQIQLSLX 660  
DB 601 VGASOMTVLSRPVMDVTLMSFSPARIPVHEVCSTSNKMKKEGNITICQIQLSLX 660  
QY 661 POFQGRVLANTLYTLQLDGHRTRRGLPPGGRHELRRIIAVTTSMSCDFFHFPPVCQD 720  
DB 661 POFQGRVLANTLYTLQLDGHRTRRGLPPGGRHELRRIIAVTTSMSCDFFHFPPVCQD 720  
QY 721 LISPINVSLNLSLMBEETPPDQAKGDIPILRPSLHSTWEIPEFKNGCEDKCKEAN 780  
DB 721 LISPINVSLNLSLMBEETPPDQAKGDIPILRPSLHSTWEIPEFKNGCEDKCKEAN 780

QY 781 LRVSFSPARALRLTFASISVELSTSNLEBDAYWVDLHFPFGISFRKVEMLKPHSQ 840  
DB 781 LRVSFSPARALRLTFASISVELSTSNLEBDAYWVDLHFPFGISFRKVEMLKPHSQ 840  
QY 841 IPVSCBELPEESRLSRALSQNVSPIFKAGSHVALQMMENLTVNSGWSGVELHANVC 900  
DB 841 IPVSCBELPEESRLSRALSQNVSPIFKAGSHVALQMMENLTVNSGWSGVELHANVC 900  
QY 901 NNEDSDLENSATTTIIPILYINILLOQEDSTLYVSFPKPKKHQVHMVQVRLOPS 960  
DB 901 NNEDSDLENSATTTIIPILYINILLOQEDSTLYVSFPKPKKHQVHMVQVRLOPS 960  
QY 961 IHDNIFTLBAVVGVPQPESEGITTHQMSVQMPBPVCHYEDLERLPDAEPCLPGALFR 1020  
DB 961 IHDNIFTLBAVVGVPQPESEGITTHQMSVQMPBPVCHYEDLERLPDAEPCLPGALFR 1020  
QY 1021 CPVVFROEILVQYIGTLELVGEIEASSMFSLCSLSISFNSSKHFLYGSNASLAQVVMK 1080  
DB 1021 CPVVFROEILVQYIGTLELVGEIEASSMFSLCSLSISFNSSKHFLYGSNASLAQVVMK 1080  
QY 1081 VDVVYERQMLLYLVLSGIGLLLLLIIFTLYLVVGPFRKRLKERMEAGRGVNPGLPAEDS 1140  
DB 1081 VDVVYERQMLLYLVLSGIGLLLLLIIFTLYLVVGPFRKRLKERMEAGRGVNPGLPAEDS 1140  
QY 1141 EQLASQGEADPGCLKPIHEKDESGGKGD 1170  
DB 1141 EQLASQGEADPGCLKPIHEKDESGGKGD 1170  
RESULT 2  
ABU05077  
ID ABU05077 standard; protein; 1170 AA.  
XX  
AC ABU05077;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1743.  
XX  
KW Translational profiling; expressed protein tag; EPT, kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN W0200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PE 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCO5 INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX  
DR WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
XX cytoskeletal proteins, receptors or transcription factors), useful for  
XX treating cancer; e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
XX leukemia.  
XX  
PS Example 2; SEQ ID NO 1743; 134pp; English.



DR N-PSDB; AAL62479.

XX New integrin alpha-L polypeptide or polynucleotide, useful for preparing  
PT a composition for treating hematological, gastrointestinal, CNS or  
PT cardiovascular disorder, asthma or COPD.

XX  
PS Claim 1; Page 106-108; 121pp; English.

CC The invention relates to human integrin alpha-L protein and its nucleic  
CC acid sequence. Integrin alpha-L DNA is used to prepare a composition for  
CC treating hematological, gastrointestinal, central nervous system (CNS)  
CC or cardiovascular disorder, asthma or chronic obstructive pulmonary  
CC disorder (COPD). It is also used in gene therapy. The present sequence is  
CC human integrin alpha-L protein. Human integrin alpha-L gene is located at  
CC chromosome 16p11.2

XX  
SQ Sequence 1170 AA;

Query Match 100.0%; Score 6106; DB 6; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPASSTYNDVGAASFSPRRGRHGRVLYGVNGVYGA 60  
DB 1 MKDSCITVMAMALLSGFFFPASSTYNDVGAASFSPRRGRHGRVLYGVNGVYGA 60  
QY PGEAGNSTSLYQCCSGTGCHLPTVLRGSNTSKYLGMFLATDPDGSILACDPGLSPKCD 120  
DB PGEAGNSTSLYQCCSGTGCHLPTVLRGSNTSKYLGMFLATDPDGSILACDPGLSPKCD 120  
QY 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVDLFLPDGSMSLQPDFQKILDFMK 180  
DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVDLFLPDGSMSLQPDFQKILDFMK 180  
QY 181 DVMKKLSNTSQPAAVGOSTSYKTEPDSYVKKRDPALLKHYKMLLNTTGALINY 240  
DB 181 DVMKKLSNTSQPAAVGOSTSYKTEPDSYVKKRDPALLKHYKMLLNTTGALINY 240  
QY 241 ATVEFBEELGARPATKVLIIITDGEATDSGNIDAAKIIIRYIGIGFQTKSQEETLH 300  
DB 241 ATVEFBEELGARPATKVLIIITDGEATDSGNIDAAKIIIRYIGIGFQTKSQEETLH 300  
QY 301 KFAKSPASEPVKIIDTFEKLKDLFTELQKIVIEGTSKODLTSPNMLSSSGISADLSR 360  
DB 301 KFAKSPASEPVKIIDTFEKLKDLFTELQKIVIEGTSKODLTSPNMLSSSGISADLSR 360  
QY 361 GHAVVAVGADWAGGLDLKADLDDTFIGNBPLTPVRAGYLGYYTWMPSRQKISL 420  
DB 361 GHAVVAVGADWAGGLDLKADLDDTFIGNBPLTPVRAGYLGYYTWMPSRQKISL 420  
QY 421 ASGA.PRYOHMGRVLLFOBPQGGHMSOVQTIHGTOIGSYFGSELGVVDODGETELLII 480  
DB 421 ASGA.PRYOHMGRVLLFOBPQGGHMSOVQTIHGTOIGSYFGSELGVVDODGETELLII 480  
QY 481 GAPLFYGEORGARVFIYORQLGFEBSVELQDPGYLGRFGAITALTDINGDLVDVA 540  
DB 481 GAPLFYGEORGARVFIYORQLGFEBSVELQDPGYLGRFGAITALTDINGDLVDVA 540  
QY 541 VGAPLEBEGAVYITNGRHGGLSPQPSQRIEQTOUTLSGTOFGRSIHGYKDLBEGDLADVA 600  
DB 541 VGAPLEBEGAVYITNGRHGGLSPQPSQRIEQTOUTLSGTOFGRSIHGYKDLBEGDLADVA 600  
QY 601 VGASQMTVLSRPVDMVTLSFSPAEIPVHBEVCSSTSNKMEGVNITTCPOIKSLY 660  
DB 601 VGASQMTVLSRPVDMVTLSFSPAEIPVHBEVCSSTSNKMEGVNITTCPOIKSLY 660  
QY 661 POFQGRVAVNTLYTQLDGRTRRRGLPPGGRHLELRNIATVTSNCTDFSFHPVAVQD 720  
DB 661 POFQGRVAVNTLYTQLDGRTRRRGLPPGGRHLELRNIATVTSNCTDFSFHPVAVQD 720  
QY 721 LISPINVSLNLSMBEETPRDQAKODIPPIILPSLSHSTWELPEFKNGCEDKCKCAN 780  
DB 721 LISPINVSLNLSMBEETPRDQAKODIPPIILPSLSHSTWELPEFKNGCEDKCKCAN 780

QY 781 LRVSFSPARARALRLTAPASLSEYLSLNLSEADAYWVQDLHPFGSLFRKVEMLKPSHQ 840  
DB 781 LRVSFSPARARALRLTAPASLSEYLSLNLSEADAYWVQDLHPFGSLFRKVEMLKPSHQ 840  
QY 841 IPVSCEELPEESRLSRALSCNVSSPIFKAGHSVALQMMNTLVNSSWSDSVELHANVC 900  
DB 841 IPVSCEELPEESRLSRALSCNVSSPIFKAGHSVALQMMNTLVNSSWSDSVELHANVC 900  
QY 901 NNEBSDLLNENSAATTIPIIYINILIQODEDSTLYVSFTPKPKKHQVHMVQVRLOPS 960  
DB 901 NNEBSDLLNENSAATTIPIIYINILIQODEDSTLYVSFTPKPKKHQVHMVQVRLOPS 960  
QY 961 IHDNIPFLBAVAVGPOPPEEGPITHOWSQVMEPPVCHIEDLERLPDAEPLPGALFR 1020  
DB 961 IHDNIPFLBAVAVGPOPPEEGPITHOWSQVMEPPVCHIEDLERLPDAEPLPGALFR 1020  
QY 1021 CPVVFROEILVQVIGTLELVGEIEASMSFSLCSLSISFNSKHFHLYGSNASTLAQVVMK 1080  
DB 1021 CPVVFROEILVQVIGTLELVGEIEASMSFSLCSLSISFNSKHFHLYGSNASTLAQVVMK 1080  
QY 1081 VDVIYERQMTLYVLSGIGILLILLIFVLYKVGFFKRLKEMAGRGVNGIPAEBS 1140  
DB 1081 VDVIYERQMTLYVLSGIGILLILLIFVLYKVGFFKRLKEMAGRGVNGIPAEBS 1140  
QY 1141 EQLASQEGADPGCLKPLHEKDSRSGGKD 1170  
DB 1141 EQLASQEGADPGCLKPLHEKDSRSGGKD 1170

RESULT 4  
ADM99587 standard; protein; 1170 AA.  
ID ADM99587;  
AC ADM99587;  
DT 17-JUN-2004 (first entry)  
XX  
DE Human integrin alphaL subunit precursor protein.  
XX  
KW integrin alpha subunit; beta; antipeptidic; thrombolytic; anticoagulant;  
KW osteopathic; cyostatic; immunosuppressive; antiinflammatory;  
KW neuroprotective; antiskinning; immunotherapy; inflammatory;  
KW autoimmune disorder; thrombosis; cancer; osteoporosis;  
KW sickle cell anaemia; psoriasis; multiple sclerosis; human; alphaL;  
KW precursor.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 214 /note= "Encoded by TGG"  
XX  
PN MO204007530-A2.  
XX  
PD 22-JAN-2004.  
XX  
PE 17-JUL-2003; 2003WO-US022301.  
XX  
PR 17-JUL-2002; 2002US-0396783P.  
PR 17-JUL-2002; 2002US-0396790P.  
PR 11-SEP-2002; 2002US-0410135P.  
XX  
PA (BL00-) CENT BLOOD RES INC.  
XX  
PI Springer TA, Takagi J;  
XX  
DR WPI: 2004-12287/12.  
DR N-PSDB; ADM99586.  
XX  
FT Novel modified integrin protein having extracellular domains of integrin  
PT alpha and beta subunits or integrin alphaI and beta3 subunit, useful for  
PT treating integrin mediated disorders.



XX Disclosure: SEQ ID NO 2; 232pp; English.  
 PS  
 XX The invention relates to a novel isolated or recombinant modified  
 CC integrin protein having extracellular domains of integrin alpha and beta  
 CC subunits where one of the subunits has one or more mutations, an altered  
 CC surface feature or an amino acid substitution or internal deletion,  
 CC extracellular domains of the integrin beta subunit that comprise a  
 CC mutation that alters a non-cysteine residue to cysteine or extracellular  
 CC domains of integrin alpha and beta subunits. The polypeptide of the  
 CC invention demonstrates antiposrotic, thrombolytic, anticoagulant,  
 CC osteoprotective, cytostatic, immunosuppressive, anti-inflammatory,  
 CC immunotherapy in order to prevent or treat an integrin-mediated disorder  
 CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,  
 CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple  
 CC sclerosis. The current sequence is that of the human integrin alpha  
 CC subunit precursor protein of the invention.

XX Sequence 1170 AA;

Query Match 100.0%; Score 6106; DB 8; Length 1170;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSCITVAMALLSGFFPAPASSYNDVRCARSPPRAGRHRYLQYNGYVGA 60  
 DB 1 MDSCITVAMALLSGFFPAPASSYNDVRCARSPPRAGRHRYLQYNGYVGA 60  
 QY 61 PGRGNSGSLYOCOSGTGHCPLTLRGSNYTSKYLGMTLATPTDGSILACPGISRTD 120  
 DB 61 PGRGNSGSLYOCOSGTGHCPLTLRGSNYTSKYLGMTLATPTDGSILACPGISRTD 120  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVLPDGSMSLQPDFOKILDFMK 180  
 DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVLPDGSMSLQPDFOKILDFMK 180  
 QY 181 DVNKLKLSNTSYOPAAVQSTSYKTEPDSYKYRKOPDALKHVGMILLNTPGAINV 240  
 DB 181 DVNKLKLSNTSYOPAAVQSTSYKTEPDSYKYRKOPDALKHVGMILLNTPGAINV 240  
 QY 181 DVNKLKLSNTSYOPAAVQSTSYKTEPDSYKYRKOPDALKHVGMILLNTPGAINV 240  
 DB 181 DVNKLKLSNTSYOPAAVQSTSYKTEPDSYKYRKOPDALKHVGMILLNTPGAINV 240  
 QY 241 ATAVFREELGAPDPAATKVLIIITDGPATSGNIDAKOIRIYIGIKGFQKESQETH 300  
 DB 241 ATAVFREELGAPDPAATKVLIIITDGPATSGNIDAKOIRIYIGIKGFQKESQETH 300  
 QY 241 ATAVFREELGAPDPAATKVLIIITDGPATSGNIDAKOIRIYIGIKGFQKESQETH 300  
 DB 241 ATAVFREELGAPDPAATKVLIIITDGPATSGNIDAKOIRIYIGIKGFQKESQETH 300  
 QY 301 KEASKPASEFVKILDTFEKLKDLFTELQKKIYIVIGKTSKODLTSFMELSSSGISADLSR 360  
 DB 301 KEASKPASEFVKILDTFEKLKDLFTELQKKIYIVIGKTSKODLTSFMELSSSGISADLSR 360  
 QY 301 KEASKPASEFVKILDTFEKLKDLFTELQKKIYIVIGKTSKODLTSFMELSSSGISADLSR 360  
 DB 301 KEASKPASEFVKILDTFEKLKDLFTELQKKIYIVIGKTSKODLTSFMELSSSGISADLSR 360  
 QY 361 GHAIVGAVGAKWAGGFLDLKADLDDPTFIGNEPPLTEVRAGYLGTVTWLPSRQTSIL 420  
 DB 361 GHAIVGAVGAKWAGGFLDLKADLDDPTFIGNEPPLTEVRAGYLGTVTWLPSRQTSIL 420  
 QY 421 ASDAPRYOMGRVLLFOEPQGGHWSQVTHGTQIGSYFGGELCGVDDODGETELLII 480  
 DB 421 ASDAPRYOMGRVLLFOEPQGGHWSQVTHGTQIGSYFGGELCGVDDODGETELLII 480  
 QY 481 GAFIFYGEORGRVETIYQRRLGFEBVSELOQDPGYLGRFEBATITALDINGDGLVVA 540  
 DB 481 GAFIFYGEORGRVETIYQRRLGFEBVSELOQDPGYLGRFEBATITALDINGDGLVVA 540  
 QY 541 GAFIFYGEORGRVETIYQRRLGFEBVSELOQDPGYLGRFEBATITALDINGDGLVVA 540  
 DB 541 GAFIFYGEORGRVETIYQRRLGFEBVSELOQDPGYLGRFEBATITALDINGDGLVVA 540  
 QY 541 VGAPLEBOGAVYIFNGRHGGLSPQPSQRIEQTQVLSGIQWFGRSIHGVKDLREGDGLADVA 600  
 DB 541 VGAPLEBOGAVYIFNGRHGGLSPQPSQRIEQTQVLSGIQWFGRSIHGVKDLREGDGLADVA 600  
 QY 601 VGASOMYIVSSRPVVDWVTLMSPAPRIPVHEVSCVSTSKMEGVNITTCPIKSLY 660  
 DB 601 VGASOMYIVSSRPVVDWVTLMSPAPRIPVHEVSCVSTSKMEGVNITTCPIKSLY 660  
 QY 661 POFQGRVAVNLTYTLQLDGHRTTRRGLFPGGHRLRNIAVTTMSCTDPSFHPVVCYQD 720  
 DB 661 POFQGRVAVNLTYTLQLDGHRTTRRGLFPGGHRLRNIAVTTMSCTDPSFHPVVCYQD 720

QY 721 LISPINVSLNFSIMEEGTPRDQROGKDIPILBPSLSHSETWEIPEKNGCEDKKCEAN 780  
 DB 721 LISPINVSLNFSIMEEGTPRDQROGKDIPILBPSLSHSETWEIPEKNGCEDKKCEAN 780  
 QY 781 LRVSPSPRSALRLTAASISVELSLNLEDAYWOLDHFPGLSPFRKVMKPPHQ 840  
 DB 781 LRVSPSPRSALRLTAASISVELSLNLEDAYWOLDHFPGLSPFRKVMKPPHQ 840  
 QY 841 IPVSCEELPEBSRLISRLSCNVSSPIFRKAGSVALQMMFNTLVNNSGDSVELHANVTC 900  
 DB 841 IPVSCEELPEBSRLISRLSCNVSSPIFRKAGSVALQMMFNTLVNNSGDSVELHANVTC 900  
 QY 901 NNEEDSLIEDNSATITIPILPINLIDODSDSTLYSFTKGPRIHVKMYQVRIQPS 960  
 DB 901 NNEEDSLIEDNSATITIPILPINLIDODSDSTLYSFTKGPRIHVKMYQVRIQPS 960  
 QY 961 IHDNHIPTLBAVGVQPPSGPITRQMSVOMEPVPCHYEDLERLPPAABPCLPALFR 1020  
 DB 961 IHDNHIPTLBAVGVQPPSGPITRQMSVOMEPVPCHYEDLERLPPAABPCLPALFR 1020  
 QY 1021 CPVFRQELIVQVIGTLELVEIEEASMSFSLCSSISISFNSSKPHLYGSNLSLAQVYMK 1080  
 DB 1021 CPVFRQELIVQVIGTLELVEIEEASMSFSLCSSISISFNSSKPHLYGSNLSLAQVYMK 1080  
 QY 1081 VDVIYKQMLTYLNLSTGIGLLLLIFIVLYKGFYKGNLKEKMEAGRGVPMNGIPADS 1140  
 DB 1081 VDVIYKQMLTYLNLSTGIGLLLLIFIVLYKGFYKGNLKEKMEAGRGVPMNGIPADS 1140  
 QY 1141 EOLASGOEAGDPGCLKPLHEKDSBSGGKD 1170  
 DB 1141 EOLASGOEAGDPGCLKPLHEKDSBSGGKD 1170

#### RESULT 5

AAR80107  
 ID AAR80107 standard; protein; 1170 AA.

XX AAR80107;

XX 04-MAR-1996 (first entry)

XX LFA-1 alpha subunit CD11a.

XX CD11a; leucocyte function-associated antigen-1; LFA-1; integrin.

OS Homo sapiens.

XX Homo sapiens.

XX Key Peptide

XX Location/Qualifiers

XX 1..25

XX /label= sig\_peptide

XX 32..79

XX /label= Repeat

XX /note= "Repeat I"

XX 82..132

XX /label= Repeat

XX /note= "Repeat II"

XX 170..349

XX /label= Idomain

XX /note= "internal domain"

XX 339..391

XX /label= Repeat

XX /note= "Repeat III"

XX 392..446

XX /label= Repeat

XX /note= "Repeat IV"

XX 447..508

XX /label= Repeat

XX /note= "Repeat V"

XX 509..567

XX /label= Repeat

XX /note= "Repeat VI"

XX 568..629

XX /label= Repeat

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FT      /note= "Repeat VII"
FT      1089..1112
FT      /label= Trans
FT      /note= "transmembrane domain"
FT      1113..1170
FT      /label= Cyto
FT      /note= "cytoplasmic domain"
XX      MO9528170-A1.
XX      26-OCT-1995.
XX      19-APR-1995; 95WO-US004886.
XX      19-APR-1994; 94US-00229513.
XX      (UNIV ) UNIV KANSAS.
XX      Benedict S, Siahaan TJ, Chan MA, Tibbette SA;
XX      WPI, 1995-373631/48.
XX      Changing peptide reactivity via conjugation with a second peptide -
XX      FT causes change in conformation of first peptide, pref. LFA-1 and ICAM-1
XX      functional domain derived peptide(s).
XX      Claim 11; Page 34-37; 64pp; English.
XX      Functional domains derived from LFA-1 alpha subunit CD11a (AAR80107), LFA
XX      CC -1 beta subunit CD18 (AAR80107) and ICAM-1 CD43 (AAR80110) are used as
XX      CC the basis of short, synthetic peptides (AAR80109, AAR80111-24) that
XX      CC modulate ICAM/LFA binding interaction. CD11a is obtd. from human PMA-
XX      CC stimulated T-lymphocyte HL-60 cells
XX      SQ Sequence 1170 AA;
Query Match 99.9%; Score 6098; DB 2; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 MKDSCITTMAMALLSGFFFPAPASYNLDVRCANSPSPRRGRHGRVYLOVGVNGVYGA 60
DB      1 MKDSCITTMAMALLSGFFFPAPASYNLDVRCANSPSPRRGRHGRVYLOVGVNGVYGA 60
QY      61 PGEKNGTSLKVCOCSTGHCCLPYTLRGSNYSKYIGMTLADPTDGSITLACDPGLSRTCD 120
DB      61 PGEKNGTSLKVCOCSTGHCCLPYTLRGSNYSKYIGMTLADPTDGSITLACDPGLSRTCD 120
QY      121 QNTYLSGLCYLFRONTLQGPMLQGRPFQECIKGNVDVFLFDGSMSTLQPDFQKILDFMK 180
DB      121 QNTYLSGLCYLFRONTLQGPMLQGRPFQECIKGNVDVFLFDGSMSTLQPDFQKILDFMK 180
QY      181 DVMTKLSTSYQFAAVQSTSYKTEFDSDYVKRQDPAALKHVKHMLLNTFGALNYV 240
DB      181 DVMTKLSTSYQFAAVQSTSYKTEFDSDYVKRQDPAALKHVKHMLLNTFGALNYV 240
QY      181 DVMTKLSTSYQFAAVQSTSYKTEFDSDYVKRQDPAALKHVKHMLLNTFGALNYV 240
DB      181 DVMTKLSTSYQFAAVQSTSYKTEFDSDYVKRQDPAALKHVKHMLLNTFGALNYV 240
QY      241 ATEVFEELGARPDPATKVLIIITDGEATDSGNIDAAKQIIIRYIIGKHFORKESQETLH 300
DB      241 ATEVFEELGARPDPATKVLIIITDGEATDSGNIDAAKQIIIRYIIGKHFORKESQETLH 300
QY      301 KFAKHPASEPVKIIDTFEKLKDLFTELQKIVLEGTSKODLTSFNMELSSSGISADLSR 360
DB      301 KFAKHPASEPVKIIDTFEKLKDLFTELQKIVLEGTSKODLTSFNMELSSSGISADLSR 360
QY      361 GHAVVGAAGADWAGGFLDLKADLDDPTFIGNEPILTEPVRAGYLGTYTWTLPSSQKISL 420
DB      361 GHAVVGAAGADWAGGFLDLKADLDDPTFIGNEPILTEPVRAGYLGTYTWTLPSSQKISL 420
QY      421 ASGARVYOHMRVLLFOEPQGGHWSOVQTHGQIGSYFGSELGQVVDQGETELLII 480
DB      421 ASGARVYOHMRVLLFOEPQGGHWSOVQTHGQIGSYFGSELGQVVDQGETELLII 480
QY      481 GAPLFYGEORGGRAVFIYQRRLQGFEEVSELQDPGYPILGRFGEAITALTIDINGDLVDVA 540

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DB      481 GAPLFYGEORGGRAVFIYQRRLQGFEEVSELQDPGYPILGRFGEAITALTIDINGDLVDVA 540
QY      541 VGAPLEBQGAVYIFNGHGGSLSPQSGRIEGTQVLSGIQWFGSS IHHVKRLBEGDLADVA 600
DB      541 VGAPLEBQGAVYIFNGHGGSLSPQSGRIEGTQVLSGIQWFGSS IHHVKRLBEGDLADVA 600
QY      601 VGASQMIYVLSRPVDMVTLMSPPAEIPVHEVECSYSTSNMKEGVNTTICFOIKSLY 660
DB      601 VGASQMIYVLSRPVDMVTLMSPPAEIPVHEVECSYSTSNMKEGVNTTICFOIKSLY 660
QY      661 PQFQRLVANLTYTLTQDGHRTRRGLFPGGRHRLRNIAVTTSMSCITDPSFHPVVCQD 720
DB      661 PQFQRLVANLTYTLTQDGHRTRRGLFPGGRHRLRNIAVTTSMSCITDPSFHPVVCQD 720
QY      721 LISPINVSLNPSLMEEGTFRDQAOQKDIPIILRPSLHETWEIIPERKXGDEKCEAN 780
DB      721 LISPINVSLNPSLMEEGTFRDQAOQKDIPIILRPSLHETWEIIPERKXGDEKCEAN 780
QY      781 LRVSPSPARSRALRLTAPASLSVELSLNLEDAVYVQLDLHPPGLSFRKVEMLKPSHQ 840
DB      781 LRVSPSPARSRALRLTAPASLSVELSLNLEDAVYVQLDLHPPGLSFRKVEMLKPSHQ 840
QY      841 IYVSCBELPEBSRLLSRALSQVSSPIFKAGHSVALQMFNTLVNSSWGDSEIHAIVTC 900
DB      841 IYVSCBELPEBSRLLSRALSQVSSPIFKAGHSVALQMFNTLVNSSWGDSEIHAIVTC 900
QY      901 NNEDSDLENSANTTIIPIIYPTNILLQDOEDSTLYVSPFKPKTHQVHMVQVRLOPS 960
DB      901 NNEDSDLENSANTTIIPIIYPTNILLQDOEDSTLYVSPFKPKTHQVHMVQVRLOPS 960
QY      961 IHDNIPITLBAVVGVPQPSBGPITTHQMSVQMEPPVCHIEDLERLPDAEPCLPGLFR 1020
DB      961 IHDNIPITLBAVVGVPQPSBGPITTHQMSVQMEPPVCHIEDLERLPDAEPCLPGLFR 1020
QY      1021 CPVVFQREILVQVIGTLELVGEIEASSMFSLCSSLSISFNSKGFHLVGSNASTLAQVVMK 1080
DB      1021 CPVVFQREILVQVIGTLELVGEIEASSMFSLCSSLSISFNSKGFHLVGSNASTLAQVVMK 1080
QY      1081 VDVVYERQMIYLYVLSGIGILLILLIFLYLYKVGFPKRLKEMKMGKRGVPGICPAEDS 1140
DB      1081 VDVVYERQMIYLYVLSGIGILLILLIFLYLYKVGFPKRLKEMKMGKRGVPGICPAEDS 1140
QY      1141 EQLASQEGADPGCLKPLHEKDSSESGGKD 1170
DB      1141 EQLASQEGADPGCLKPLHEKDSSESGGKD 1170
RESULT 6
ABB76377
ID ABB76377 standard; protein; 1170 AA.
AC ABB76377;
DPT 22-AUG-2002 (first entry)
XX      Lymphocyte function associated antigen-1.
XX      Lymphocyte function associated antigen-1; LFA-1; human;
XX      alpha/beta protein; ligand binding.
XX      Homo sapiens.
FH      Key Location/Qualifiers
FT      153..332
FT      /label= I_domain
PN      MO200231511-A2.
XX      18-APR-2002.
PD      12-OCT-2001; 2001WO-US032047.

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PR 12-OCT-2000; 2000US-0239750P.  
 XX (ICOS-) ICOS CORP.  
 PA Stauton DE;  
 PI WPI; 2002-471361/50.  
 DR  
 XX  
 XX  
 PT Modulating binding interactions between alpha/beta proteins comprising  
 PT allosteric regulatory sites, and a binding partner, by contacting with an  
 CC allosteric effector molecule that interacts with the regulatory site.  
 PS Disclosure: Fig 2; 163pp; English.  
 CC  
 CC The present sequence is the protein sequence of lymphocyte function  
 CC associated antigen-1 (LFA-1), which includes an integrin (I) domain. The  
 CC invention provides methods of modulating the binding interaction of a  
 CC first molecule, which is not LFA-1 or an I domain-containing fragment of  
 CC LFA-1, and a binding partner. The first molecule has an alpha/beta domain  
 CC structure comprising an allosteric regulatory site. Modulation of the  
 CC binding interaction involves contacting with an allosteric effector  
 CC molecule that interacts with the regulatory site. In vivo methods are  
 CC expected to alleviate and/or prevent pathological states arising from  
 CC aberrant binding activity. Methods for identifying modulators are also  
 CC provided  
 CC  
 SQ Sequence 1170 AA;  
 Query Match 99.9%; Score 6098; DB 5; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 601 VGABSQMIVLSSRPVDMVTLMSPFAPIPVHEVCSYSTSNKMEGNVITTCPIQISLY 660  
 QY 661 PFGGRIVANITTYTLQDGHRTRRRGLEPPGRHRLRNIAVTTSMCTDSFHPVVCVD 720  
 DB 661 PFGGRIVANITTYTLQDGHRTRRRGLEPPGRHRLRNIAVTTSMCTDSFHPVVCVD 720  
 QY 721 LISPINVSINSLWEESTPPDQAOQKDIPPIILRPSLHSTFWELPREKNGGEKKCAN 780  
 DB 721 LISPINVSINSLWEESTPPDQAOQKDIPPIILRPSLHSTFWELPREKNGGEKKCAN 780  
 QY 781 LRVSPSPASRALRLTAPASLVEISLSNLEEDAWVQDLHPFGGLSFRKYMELKPHSQ 840  
 DB 781 LRVSPSPASRALRLTAPASLVEISLSNLEEDAWVQDLHPFGGLSFRKYMELKPHSQ 840  
 QY 841 IPVSCBELPEBSRLISRALSCNVSPIFKAGHSVALQMMNTLVNSWGDVBLHANVTC 900  
 DB 841 IPVSCBELPEBSRLISRALSCNVSPIFKAGHSVALQMMNTLVNSWGDVBLHANVTC 900  
 QY 901 NNEDSDLEDNSATTIIPILPINILIODQEDSTLYVSFTPKGPKIHQVKMYQVRIOPS 960  
 DB 901 NNEDSDLEDNSATTIIPILPINILIODQEDSTLYVSFTPKGPKIHQVKMYQVRIOPS 960  
 QY 961 IHDNIPITLNAVGVPOPSRGPITTHQMSYOMBPVPCHYEDLRLPDAAEPCLPALFR 1020  
 DB 961 IHDNIPITLNAVGVPOPSRGPITTHQMSYOMBPVPCHYEDLRLPDAAEPCLPALFR 1020  
 QY 1021 CPVVFROBILVOVITGLVLEIEASMSFSLCSSLSISFNSSKPHLGSNASTLAQVVMK 1080  
 DB 1021 CPVVFROBILVOVITGLVLEIEASMSFSLCSSLSISFNSSKPHLGSNASTLAQVVMK 1080  
 QY 1081 VDVTYRKQMLTYLYLSGIGLLILLFTVLYKVGFFKRNILKEKMEAGRGVPNGI PAEDS 1140  
 DB 1081 VDVTYRKQMLTYLYLSGIGLLILLFTVLYKVGFFKRNILKEKMEAGRGVPNGI PAEDS 1140  
 QY 1141 BQLASGOEAGDPGCLKPLHERDSGSGGKD 1170  
 DB 1141 BQLASGOEAGDPGCLKPLHERDSGSGGKD 1170

RESULT 7  
 ABU05076  
 ID ABU05076 standard; protein. 1170 AA.  
 XX  
 XX ABU05076;  
 AC  
 XX  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Human expressed protein tag (BPT) #1742.  
 XX  
 XX Translational profiling; expressed protein tag; BPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200278524-A2.  
 PN  
 XX  
 PD 10-OCT-2002.  
 XX  
 XX  
 PF 28-MAR-2002; 2002WO-US009671.  
 XX  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 XX  
 PA (ZYCO-) ZYCO INC.



XX (ZYCO-) ZYCO INC.  
 PA  
 XX Chicz RM, Tomlinson AJ, Urban RG;  
 PI WPI, 2003-040607/03.  
 DR  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT creating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 PS Example 2; SEQ ID NO 1739; 134pp; English.  
 CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1170 AA;  
 Query Match 99.9%; Score 6098; DB 6; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 541 VGAPLEBQAGAVYINGRHGSLSPQSORIESTOVLSGIQWFRGSIHGKYLBSGDLADVA 600  
 DB 541 VGAPLEBQAGAVYINGRHGSLSPQSORIESTOVLSGIQWFRGSIHGKYLBSGDLADVA 600  
 QY 601 VGASQMIIVLSRRPVDMVTLMSPSPAEIPVHEVCSYSTSNKKKEGVNITICQIKSLY 660  
 DB 601 VGASQMIIVLSRRPVDMVTLMSPSPAEIPVHEVCSYSTSNKKKEGVNITICQIKSLY 660  
 QY 661 POFQGRIVANVTYTLQDGHRTRRRGLPPGGRHRLRNIAVTTSMSCSTDSPFHPVCYQD 720  
 DB 661 POFQGRIVANVTYTLQDGHRTRRRGLPPGGRHRLRNIAVTTSMSCSTDSPFHPVCYQD 720  
 QY 721 LISPIVNSLNSLWEEBETPPDOAOGNDIPILRPSLHSTWTIIPFKNGGDKCCAN 780  
 DB 721 LISPIVNSLNSLWEEBETPPDOAOGNDIPILRPSLHSTWTIIPFKNGGDKCCAN 780  
 QY 781 LRVFSPSPARSLALTLTAPASLVSLSNLEEDAYWQDLHFPFGLSFRKYEMLKPHSQ 840  
 DB 781 LRVFSPSPARSLALTLTAPASLVSLSNLEEDAYWQDLHFPFGLSFRKYEMLKPHSQ 840  
 QY 841 IPVSCBELPESRLLSLRSLSCNVSSPIFKAGSHVALQWMENTLVNSWGSVELHANVTC 900  
 DB 841 IPVSCBELPESRLLSLRSLSCNVSSPIFKAGSHVALQWMENTLVNSWGSVELHANVTC 900  
 QY 901 NNEBSDLLEDSATTTIPIILPINILIDQDSDTLVYSPFKGPKIHQVKMYOVRLOPS 960  
 DB 901 NNEBSDLLEDSATTTIPIILPINILIDQDSDTLVYSPFKGPKIHQVKMYOVRLOPS 960  
 QY 961 IHDNIPITLNAVGVPOPSRGPITTHQMSVMEPPVPCHEYDRLRLPDAAPCPLGALFR 1020  
 DB 961 IHDNIPITLNAVGVPOPSRGPITTHQMSVMEPPVPCHEYDRLRLPDAAPCPLGALFR 1020  
 QY 1021 CPVVFROELIVQVIGTELVEIEASSMFSLCSSLSISFNSKPHLYGSNASTLAQVVMK 1080  
 DB 1021 CPVVFROELIVQVIGTELVEIEASSMFSLCSSLSISFNSKPHLYGSNASTLAQVVMK 1080  
 QY 1081 VDVVYRKOMLYLYLSGIGILLILLIFIVLYKVGFFKRNKEMKMEAGRVPNGI PAEDS 1140  
 DB 1081 VDVVYRKOMLYLYLSGIGILLILLIFIVLYKVGFFKRNKEMKMEAGRVPNGI PAEDS 1140  
 QY 1141 EQLASGOEAGDPGCLKPLHEKDSGSGGKD 1170  
 DB 1141 EQLASGOEAGDPGCLKPLHEKDSGSGGKD 1170

RESULT 9  
 AB05071  
 ID AB05071 standard; protein; 1170 AA.  
 XX  
 AC AB05071;  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Human expressed protein tag (EPT) #1737.  
 XX  
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002WO-US009671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
XX (ZYCO-) ZYCOS INC.  
XX  
XX Chicx RM, Tomlinson AJ, Urban RG;  
XX  
XX MPI, 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
XX cytoskeletal proteins, receptors or transcription factors), useful for  
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
XX leukemia.

PS Example 2; SEQ ID NO 1737; 134dp; English.

CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EBP) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1170 AA;

Query Match 99.9%; Score 6098; DB 6; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCTIVAMALLSGFFFPASSYNDVVGARSFSPRRGRHGVYLVQNGVYVGA 60  
DB 1 MKDSCTIVAMALLSGFFFPASSYNDVVGARSFSPRRGRHGVYLVQNGVYVGA 60  
QY 61 PGEBSNSTSLVQCCSGTGHCLPVTLRGNSNTSKYLGMTLADPTDGSILACDPGLSRCD 120  
DB 61 PGEBSNSTSLVQCCSGTGHCLPVTLRGNSNTSKYLGMTLADPTDGSILACDPGLSRCD 120  
QY 121 QNTYLSGLCYLFRONTLOQPMLOQRGPOECIKGNVDLVFLPDGSMLOPDEFOKILDFMK 180  
DB 121 QNTYLSGLCYLFRONTLOQPMLOQRGPOECIKGNVDLVFLPDGSMLOPDEFOKILDFMK 180  
QY 181 DVMKLSTNTSYQPAVQSTSYKTEFDSYVKRDPALLKHYVGMMLLNTFGAINVY 240  
DB 181 DVMKLSTNTSYQPAVQSTSYKTEFDSYVKRDPALLKHYVGMMLLNTFGAINVY 240  
QY 241 ATEVFRRELGARPATKYLIIITDGEATDSGNIDAOKIIRYIIGIGHFQTKSQETLH 300  
DB 241 ATEVFRRELGARPATKYLIIITDGEATDSGNIDAOKIIRYIIGIGHFQTKSQETLH 300  
QY 301 KFAKRPASEFVKIDTFEKLKDLFTELQKTYIVIEGTSKODLTSFNMELSSSGISADLSR 360  
DB 301 KFAKRPASEFVKIDTFEKLKDLFTELQKTYIVIEGTSKODLTSFNMELSSSGISADLSR 360  
QY 361 GHAVGAVGADWAGGFLDLKADLQDDTFIGNEPITPEVRAGYLGTYTWPSPRQKSTLL 420  
DB 361 GHAVGAVGADWAGGFLDLKADLQDDTFIGNEPITPEVRAGYLGTYTWPSPRQKSTLL 420  
QY 421 ASGAPRYOHMRVULLFOBPQGGHMSQVYTHGTQIGSYFGGELCGVDVDDGETELLLI 480  
DB 421 ASGAPRYOHMRVULLFOBPQGGHMSQVYTHGTQIGSYFGGELCGVDVDDGETELLLI 480

QY 481 GAPLFYGEORGGRVFIYQRRQLGFEVESEILQDPCGYPLGRFGAITALTDINGDLVDA 540  
DB 481 GAPLFYGEORGGRVFIYQRRQLGFEVESEILQDPCGYPLGRFGAITALTDINGDLVDA 540  
QY 541 VGAPLEQGAIVYIFNGHGGSLSPQSORIGTOVLSGIQWFGNSIHGVKDLBGDLADVA 600  
DB 541 VGAPLEQGAIVYIFNGHGGSLSPQSORIGTOVLSGIQWFGNSIHGVKDLBGDLADVA 600  
QY 601 VGAESQMIIVLSRRVVMVMTLMSFSPAETPVHRECSYSTSNMKKEVNTITCQIKSLY 660  
DB 601 VGAESQMIIVLSRRVVMVMTLMSFSPAETPVHRECSYSTSNMKKEVNTITCQIKSLY 660  
QY 661 POFQGRIVANLTYTLQDGHRTTRRGLPFGGRHRLRNIAVTTSMSCSTDSPFHPVCVD 720  
DB 661 POFQGRIVANLTYTLQDGHRTTRRGLPFGGRHRLRNIAVTTSMSCSTDSPFHPVCVD 720  
QY 721 LISPINVSLNPSLMEEGTFRDQAGKDIPIILRPSLSEETWEIPPEKNCGEDKCEAN 780  
DB 721 LISPINVSLNPSLMEEGTFRDQAGKDIPIILRPSLSEETWEIPPEKNCGEDKCEAN 780  
QY 781 LRVSFSPARRALRTAPASLSELSLSEEDAYWQDLHPPGISFPRKVMKLPKHSQ 840  
DB 781 LRVSFSPARRALRTAPASLSELSLSEEDAYWQDLHPPGISFPRKVMKLPKHSQ 840  
QY 841 IPVSCBELPESRRLSRALSCNVSPIFKAGHSVALQMFNTLVNSGDSVIELHANVTC 900  
DB 841 IPVSCBELPESRRLSRALSCNVSPIFKAGHSVALQMFNTLVNSGDSVIELHANVTC 900  
QY 901 NNEDSDILENSATTIIPILPINILIQODEDSTLYVSPFKGPKIHQVHMTQVRIOPS 960  
DB 901 NNEDSDILENSATTIIPILPINILIQODEDSTLYVSPFKGPKIHQVHMTQVRIOPS 960  
QY 961 IHDNITLRAVYGVPPSPSGPTTHQWSQVMPVPCHEDELRIPDAABPCLPGALFR 1020  
DB 961 IHDNITLRAVYGVPPSPSGPTTHQWSQVMPVPCHEDELRIPDAABPCLPGALFR 1020  
QY 1021 CPVVFROEILVOVIGTLEVGIEIASMSFSLCSLSISFNSKHFLHLYGSNASLAQVVMK 1080  
DB 1021 CPVVFROEILVOVIGTLEVGIEIASMSFSLCSLSISFNSKHFLHLYGSNASLAQVVMK 1080  
QY 1081 VDVYERKQMTLYLYLSGIGGLLLLLIFLYLYVGFPRKMLKERMEAGGVNGIPEADS 1140  
DB 1081 VDVYERKQMTLYLYLSGIGGLLLLLIFLYLYVGFPRKMLKERMEAGGVNGIPEADS 1140  
QY 1141 EQLASQEGADPGCLRPLHEKDSBSGGKD 1170  
DB 1141 EQLASQEGADPGCLRPLHEKDSBSGGKD 1170

RESULT 10  
ADO43837 standard; protein; 1170 AA.  
XX  
XX ADO43837;  
XX  
XX 15-JUL-2004 (first entry)  
XX  
XX Human lymphocyte function-associated antigen alpha subunit.  
XX  
XX Human lymphocyte function-associated antigen; LFA-1; alpha subunit;  
XX adhesion molecule; cell-cell interaction; inflammation;  
XX cytotoxic T lymphocyte; CTL-mediated cell lysis; chronic viral hepatitis;  
XX autoimmune disorder; HIV infection; AIDS;  
XX acquired immunodeficiency syndrome; CD4+ cell; antibody; Sef1; TSG/4;  
XX propeller domain; CD11a; immunogen.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX  
XX Key Location/Qualifiers  
XX Domain 26..614  
XX /label = Propeller\_domain  
XX  
XX US2004062765-A1.

XX 01-APR-2004.  
 PD 27-SEP-2002; 2002US-00261164.  
 XX 27-SEP-2002; 2002US-00261164.  
 PR 27-SEP-2002; 2002US-00261164.  
 XX (KAPU/) KAPUSTAY P M.  
 PA (LEWIS/) LEWIS R H.  
 PI Kapustay PM, Lewis RH;  
 DR WPI: 2004-294382/27.  
 DR N-PSDB: ADO43839.  
 PT Use of an anti lymphocyte function-associated antigen 1 alpha subunit  
 PT (CD11a) antibody for treating a subject having or at risk of having a  
 PT physiological condition associated with or caused by decreased CD4+ cell  
 PT numbers, e.g. HIV.  
 XX  
 PS Disclosure; SEQ ID NO 1; 23pp; English.  
 CC The invention relates to treating a subject having or at risk of having a  
 CC physiological condition associated with or caused by decreased CD4+ cell  
 CC numbers, comprising administering an antibody that binds to lymphocyte  
 CC function-associated antigen 1 (LFA-1) alpha subunit (CD11a) in an amount  
 CC greater than 1 mg/kg body weight. LFA-1 is an adhesion molecule involved  
 CC in cell-cell interaction, inflammation, cytotoxic T lymphocyte (CTL)-  
 CC mediated cell lysis and implicated in chronic viral hepatitis, autoimmune  
 CC disorders and HIV infection (AIDS, acquired immunodeficiency syndrome).  
 CC Also included are a composition comprising 100 mg or more S6p1, TS2/4  
 CC antibody (humanized form or its subsequence) and a pharmaceutical  
 CC carrier, a composition comprising 100 mg or more fully human antibody  
 CC having a binding affinity for LFA-1 alpha subunit (or an epitope in LFA-1  
 CC alpha subunit) within about 1-100 of the binding affinity of S6p1 or  
 CC TS2/4 (and a pharmaceutical carrier) and a kit comprising a composition  
 CC above, which is in a single unit dosage form for administration to a  
 CC subject. The antibody inhibits binding of S6p1 or TS2/4 antibody to LFA-1  
 CC alpha subunit, or binds to an epitope to which S6p1 or TS2/4 antibody  
 CC binds, where the epitope comprises an LFA-1 alpha subunit propeller  
 CC domain and is located all or in a part of amino acids 1-57 of the LFA-1  
 CC alpha subunit comprising a sequence of ADO4383. The method is useful for  
 CC increasing CD4+ cell numbers in a subject, for inhibiting or preventing  
 CC decreases in CD4+ cell numbers in a subject, useful for treating a  
 CC subject exposed to HIV or at risk of exposure to HIV. The present  
 CC sequence is the human LFA-1 alpha subunit (CD11a) protein.  
 CC  
 XX  
 SQ Sequence 1170 AA;  
 Query Match 99.9%; Score 6098; DB 8; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 301 KPASKPASEPVKILIDTFEKLKDLPTELQKTIYVIGTSKODLTSPNMLSSSGISADLSR 360  
 DB 301 KPASKPASEPVKILIDTFEKLKDLPTELQKTIYVIGTSKODLTSPNMLSSSGISADLSR 360  
 QY 361 GHAIVGAVGAKDMAGGFADLKADLDDDFEIGNEPILTPFVRAGYGYATYTWLPSPROKSTLL 420  
 DB 361 GHAIVGAVGAKDMAGGFADLKADLDDDFEIGNEPILTPFVRAGYGYATYTWLPSPROKSTLL 420  
 QY 421 ASGARVYOMGRVILLPOBPQGGHMSQVQTIHGTOIGSYFGGELCGVDVDDGSETELLII 480  
 DB 421 ASGARVYOMGRVILLPOBPQGGHMSQVQTIHGTOIGSYFGGELCGVDVDDGSETELLII 480  
 QY 481 GAPLFGGORGGRVPTIYRRLQGFBEVSELQGDDEYPLGRGGEALTALTDINGDLVYVA 540  
 DB 481 GAPLFGGORGGRVPTIYRRLQGFBEVSELQGDDEYPLGRGGEALTALTDINGDLVYVA 540  
 QY 541 VGAPLEEGQAYIIFNGRGGHSGPOPSQRIEGQVLSGIQWGRSHGVKDLBGDLADVA 600  
 DB 541 VGAPLEEGQAYIIFNGRGGHSGPOPSQRIEGQVLSGIQWGRSHGVKDLBGDLADVA 600  
 QY 601 VGASQMIIVLSRPVDMVTLMSPSPAEIPVHEVECSYSTSNKMEGVNITICPOIKSLY 660  
 DB 601 VGASQMIIVLSRPVDMVTLMSPSPAEIPVHEVECSYSTSNKMEGVNITICPOIKSLY 660  
 QY 661 POFQGRVYANITITLQLDGHRTRRRGLPFGGRHRLRNIAVTTSMSCITDSEFHPVCYQD 720  
 DB 661 POFQGRVYANITITLQLDGHRTRRRGLPFGGRHRLRNIAVTTSMSCITDSEFHPVCYQD 720  
 QY 721 LISPIVNSLANSMBEESTPPDORAQGDIPILIPSLHSHTWELPEKNGGEMDKCAN 780  
 DB 721 LISPIVNSLANSMBEESTPPDORAQGDIPILIPSLHSHTWELPEKNGGEMDKCAN 780  
 QY 781 LRVSFSPASRALRLTAASISVELSLSNLEBDAYWQLDLHPPGSLFRKYMELKPHSQ 840  
 DB 781 LRVSFSPASRALRLTAASISVELSLSNLEBDAYWQLDLHPPGSLFRKYMELKPHSQ 840  
 QY 841 IPVSCBELPEESRLISRALSNVSSPIFKAGHSVALQMMFNTLVNSSWGSDELHANYTC 900  
 DB 841 IPVSCBELPEESRLISRALSNVSSPIFKAGHSVALQMMFNTLVNSSWGSDELHANYTC 900  
 QY 901 NNEOSDLLEDSATITIPILYPINILITODQDSTLYVSTFKGKIHQVKMYOVRLOPS 960  
 DB 901 NNEOSDLLEDSATITIPILYPINILITODQDSTLYVSTFKGKIHQVKMYOVRLOPS 960  
 QY 961 IHDNIPITLBAVYVQPPSPSGPITTHQMSVOMEPVPCHYEDLRLPPAAEPCLPGALFR 1020  
 DB 961 IHDNIPITLBAVYVQPPSPSGPITTHQMSVOMEPVPCHYEDLRLPPAAEPCLPGALFR 1020  
 QY 1021 CPVVFROEILVQVIGTLELVEIEASSWFSICSSLSISFNSSKHPLYGSNASILAQVVMK 1080  
 DB 1021 CPVVFROEILVQVIGTLELVEIEASSWFSICSSLSISFNSSKHPLYGSNASILAQVVMK 1080  
 QY 1081 VDVIYERQMLLYLISGIGGLLILLLIFIVYXKGFPRRNKKEKMEAGRGVPGNIPADS 1140  
 DB 1081 VDVIYERQMLLYLISGIGGLLILLLIFIVYXKGFPRRNKKEKMEAGRGVPGNIPADS 1140  
 QY 1141 EQLASGOBAGDPGCLKPLHEKDSGGGKD 1170  
 DB 1141 EQLASGOBAGDPGCLKPLHEKDSGGGKD 1170  
 RESULT 11  
 ADP12998  
 ID ADP12998 standard; protein, 1170 AA.  
 XX  
 AC ADP12998;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Protein encoding reference mRNA sequence #83.  
 XX  
 DE transplant rejection; immune system; rheumatoid arthritis; lupus;  
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.  
 KW



XX Homo sapiens.  
 OS MO2004042346-A2.  
 XX 21-MAY-2004.  
 XX 24-APR-2003; 2003WO-US012946.  
 XX 24-APR-2002; 2002US-00131831.  
 XX 20-DEC-2002; 2002US-00325899.  
 XX (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;  
 PI Rosenberg S;  
 XX WPI: 2004-400724/37.  
 DR  
 XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,  
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant  
 PT rejection, in an individual, comprises detecting the expression level of  
 PT the genes.  
 PS Claim 65; SEQ ID NO 3007; 1762bp; English.  
 XX  
 CC The present invention relates to diagnosing or monitoring transplant  
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual  
 CC comprising detecting the expression level of one or more genes. The  
 CC methods, system and kits are useful in diagnosing or monitoring  
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic  
 CC islet, lung, bone marrow or stem cell transplant rejection,  
 CC xenotransplant rejection or mechanical organ replacement rejection, in an  
 CC individual. The method is also useful in assessing the immune status of  
 CC an individual. The methods are also useful in diagnosing and monitoring  
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,  
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or  
 CC viral, bacterial or fungal infection. The present sequence represents a  
 CC protein encoded by an mRNA sequence of the invention which show altered  
 CC expression in renal transplantation and expression.  
 XX  
 SQ Sequence 1170 AA;  
 Query Match 99.9%; Score 6098; DB 8; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKDLCITTMAMALLSGFFFPAPASSYNTDVGARSFSPRAGRHFGRVLYOYGNQVYIGA 60  
 DB 1 MKDLCITTMAMALLSGFFFPAPASSYNTDVGARSFSPRAGRHFGRVLYOYGNQVYIGA 60  
 QY 61 PGEANSTGSLVQCCSGTGHCPLVTLRGSNYTSKYLGMTLADPTDGSIIACDPGLSRCTD 120  
 DB 61 PGEANSTGSLVQCCSGTGHCPLVTLRGSNYTSKYLGMTLADPTDGSIIACDPGLSRCTD 120  
 QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPFQECIKGNVLDVLFDFGSMNSLOPDEFOKILDPMK 180  
 DB 121 QNTYLSGLCYLFRONTLQGPMLQGRPFQECIKGNVLDVLFDFGSMNSLOPDEFOKILDPMK 180  
 QY 181 DVMKLSTNTSTQFAAVQFSTSTKTEFPDSDYKWKDPALAKHVGMMLLNTFGAINVY 240  
 DB 181 DVMKLSTNTSTQFAAVQFSTSTKTEFPDSDYKWKDPALAKHVGMMLLNTFGAINVY 240  
 QY 241 ATEVERRELGARPDATKYLIIITDGEATDSCNIDAKOIRITIGIGHFORKESQETLH 300  
 DB 241 ATEVERRELGARPDATKYLIIITDGEATDSCNIDAKOIRITIGIGHFORKESQETLH 300  
 QY 301 KFAKRPASEFYKILDTPEKLDLFTLEOKKIYVIGTSKODLTSFNMELSSSGISADLSR 360  
 DB 301 KFAKRPASEFYKILDTPEKLDLFTLEOKKIYVIGTSKODLTSFNMELSSSGISADLSR 360  
 QY 361 GHAVVGAAGADMGAGFLDLKADLQDDTFIGNEPVLTPEVRAGYLGYYTWTLSRQKTSLL 420  
 DB 361 GHAVVGAAGADMGAGFLDLKADLQDDTFIGNEPVLTPEVRAGYLGYYTWTLSRQKTSLL 420

DB 361 GHAVVGAAGADMGAGFLDLKADLQDDTFIGNEPVLTPEVRAGYLGYYTWTLSRQKTSLL 420  
 QY 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVOTIHGTQISYFGELGVDVDDGETELLII 480  
 DB 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVOTIHGTQISYFGELGVDVDDGETELLII 480  
 QY 481 GAPLFYGBQGRGVFIYQRRQLGFEVSELOQDGYLGRGFAITALTINDGDLVDA 540  
 DB 481 GAPLFYGBQGRGVFIYQRRQLGFEVSELOQDGYLGRGFAITALTINDGDLVDA 540  
 QY 541 VGAPLEEQGANVYIENGHHGGLSPQSORIGTQVLSGIQWFRGRIHVKOLEGGLADVA 600  
 DB 541 VGAPLEEQGANVYIENGHHGGLSPQSORIGTQVLSGIQWFRGRIHVKOLEGGLADVA 600  
 QY 601 VGASOMIVLSSRPVVMVMTLMSFSPABIPVHEVSCSYSTSNKKKEGNITICQIKSLY 660  
 DB 601 VGASOMIVLSSRPVVMVMTLMSFSPABIPVHEVSCSYSTSNKKKEGNITICQIKSLY 660  
 QY 661 PQFGRLVANITTYTLQDGHKTRRRGLPQGRHBLRNIAVTTSMSCCTDPSFHPVVCVD 720  
 DB 661 PQFGRLVANITTYTLQDGHKTRRRGLPQGRHBLRNIAVTTSMSCCTDPSFHPVVCVD 720  
 QY 721 LISPINLSNLSMEEGTSPDQAOQKDIPIILRPSLHETWRIPEKNGEDKCEAN 780  
 DB 721 LISPINLSNLSMEEGTSPDQAOQKDIPIILRPSLHETWRIPEKNGEDKCEAN 780  
 QY 781 LRVSFSPARSALRLTAPASIVSELSNLEBDAYVWQDLHFPFPGLSFRKVEMLKPSHQ 840  
 DB 781 LRVSFSPARSALRLTAPASIVSELSNLEBDAYVWQDLHFPFPGLSFRKVEMLKPSHQ 840  
 QY 841 IPVSCEELPEBSRLLSBALSCNVSPIFKAGHSVALQMMFNTLVNSSWGDSEIHAVTC 900  
 DB 841 IPVSCEELPEBSRLLSBALSCNVSPIFKAGHSVALQMMFNTLVNSSWGDSEIHAVTC 900  
 QY 901 NNEBSDLLENSSATITPIILYPINILQDOEDSTLYSFTPKGRKHQVGMVYRQPS 960  
 DB 901 NNEBSDLLENSSATITPIILYPINILQDOEDSTLYSFTPKGRKHQVGMVYRQPS 960  
 QY 961 IHDNIPFLBAVGVPPQPSBGPITTHQMSVQMEPPVCHIEDLERLDAAEPCLPGLAFR 1020  
 DB 961 IHDNIPFLBAVGVPPQPSBGPITTHQMSVQMEPPVCHIEDLERLDAAEPCLPGLAFR 1020  
 QY 1021 CPVVFROEIIIVQITLIEVGEIBASSMFSLCSSLSISFNSSKHFLYGSNASTLAQVVMK 1080  
 DB 1021 CPVVFROEIIIVQITLIEVGEIBASSMFSLCSSLSISFNSSKHFLYGSNASTLAQVVMK 1080  
 QY 1081 VDVIYERQMLYLYLSGIGILLLLLFYLYXKGFPRKRLKEMEAGRGVPGNIPAEBS 1140  
 DB 1081 VDVIYERQMLYLYLSGIGILLLLLFYLYXKGFPRKRLKEMEAGRGVPGNIPAEBS 1140  
 QY 1141 EQLASQGBAGDPGCLKPLHEKDSSEGGKD 1170  
 DB 1141 EQLASQGBAGDPGCLKPLHEKDSSEGGKD 1170  
 RESULT 12  
 ID ADQ39425  
 ID ADQ39425 standard; protein; 1170 AA.  
 AC ADQ39425;  
 DT 18-NOV-2004 (first entry)  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1088.  
 XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
 KW cardiant; gene therapy; human.  
 OS Homo sapiens.  
 XX MO2004058052-A2.  
 XX 15-JUL-2004.



XX 22-DEC-2003; 2003W0-US040978.  
 XX  
 PR 20-DEC-2002; 2002US-0434778P.  
 PR 10-MAR-2003; 2003US-0453135P.  
 PR 30-APR-2003; 2003US-0466412P.  
 PR 23-SEP-2003; 2003US-0504955P.  
 XX  
 PA (APPL-) APPLERA CORP.  
 XX  
 XX  
 PI Cargill M, Devlin JF, Yakubova O;  
 XX  
 DR WPI: 2004-533949/51.  
 DR N-PSDB; ADQ38597.  
 XX  
 XX Identifying an individual who has an altered risk for developing  
 PT myocardial infarction by detecting a single nucleotide polymorphism in  
 PT the individual's nucleic acids.

Query Match	99.9%	Score 6098	DB 8	Length 1170
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1169	Conservative	0	Mismatches 1	Indels 0
			Gaps 0	
Qy	1 MKDSCITWMAAMLLSGFFFPAPASSYNNLDVRARSFSPRARHRYLVQNGVYIGA	60		
Db	1 MKDSCITWMAAMLLSGFFFPAPASSYNNLDVRARSFSPRARHRYLVQNGVYIGA	60		
Qy	61 PGRGNSTSLVQCGSGTGHCIPVTLRGSNYTSKYLGMTLATPTDGSILACDPGLSRCTD	120		
Db	61 PGRGNSTSLVQCGSGTGHCIPVTLRGSNYTSKYLGMTLATPTDGSILACDPGLSRCTD	120		
Qy	121 QNTYISGLCYLFRQMLQGRGFQECIKGANDVPLPFGSMSLQPDFEQKILDFPK	180		
Db	121 QNTYISGLCYLFRQMLQGRGFQECIKGANDVPLPFGSMSLQPDFEQKILDFPK	180		
Qy	181 DVNKLSTNSYQFAVQFSTSYKTEFDSYDYKRDPDALLGHVGHMLLTNTFGAINVY	240		
Db	181 DVNKLSTNSYQFAVQFSTSYKTEFDSYDYKRDPDALLGHVGHMLLTNTFGAINVY	240		
Qy	241 ATEVERBELGARDPAITKVLIITTDGATDGSNIDAKDIIRYIIIGIKHFOTKESQETLL	300		

Dd	241	ATEVREBELGARPDATKVLIIITDGBATDSGNIIDAKOIRIYIGIKHPIQTMEQETLLH	300
Qy	301	KFASPRPASEFVKLIDTFPEKLDLFTLQKTIYVIGSTSKODLTSPFMELSSSGISADLSR	360
Dd	301	KFASPRPASEFVKLIDTFPEKLDLFTLQKTIYVIGSTSKODLTSPFMELSSSGISADLSR	360
Qy	361	GHAUVGAVGAKDMAGGFLDKADLDDPTIGNEPLTPREAAVLGTYVMWLPBROKTSLL	420
Dd	361	GHAUVGAVGAKDMAGGFLDKADLDDPTIGNEPLTPREAAVLGTYVMWLPBROKTSLL	420
Qy	421	ASGARPYOHMGVRLVLFQEPQGGGSHMSQVOTIHGTOIGSFEGGELCGVDVDDQDETELLLI	480
Dd	421	ASGARPYOHMGVRLVLFQEPQGGGSHMSQVOTIHGTOIGSFEGGELCGVDVDDQDETELLLI	480
Qy	481	GAPLPYGEORGGRVETIYORQLGFREVSHELQDPCGYPLGRFGBAITATLTDINDGLVDVA	540
Dd	481	GAPLPYGEORGGRVETIYORQLGFREVSHELQDPCGYPLGRFGBAITATLTDINDGLVDVA	540
Qy	541	VGAPLPEEGQAVYTFNGRHGGLSPPSPSORIEGTQVLSGIOMFGRSIHGVYDLBEGGLADVA	600
Dd	541	VGAPLPEEGQAVYTFNGRHGGLSPPSPSORIEGTQVLSGIOMFGRSIHGVYDLBEGGLADVA	600
Qy	601	VGASEQMIVLSRRPVMDWTLMSPSPAEIPVHEVEGVSYSNMGKGNVITTCFOIKSLY	660
Dd	601	VGASEQMIVLSRRPVMDWTLMSPSPAEIPVHEVEGVSYSNMGKGNVITTCFOIKSLI	660
Qy	661	POFQORLVANLTYYTLQDGHRTRRRGLPFGGHELRRLNAVTTSMGCTSPSFFHPPCVOD	720
Dd	661	POFQORLVANLTYYTLQDGHRTRRRGLPFGGHELRRLNAVTTSMGCTSPSFFHPPCVOD	720
Qy	721	LISPIVNSLNFSLMEEBEGTPRDQRAQKQDIPILRPSLHSEFWIIPFEKNCGEDKCEAN	780
Dd	721	LISPIVNSLNFSLMEEBEGTPRDQRAQKQDIPILRPSLHSEFWIIPFEKNCGEDKCEAN	780
Qy	781	LRVSSSPARSRLRLTAFASSLVSELSNLEEDAWVQUDLHPRPGLSFRKYEMLKPHSQ	840
Dd	781	LRVSSSPARSRLRLTAFASSLVSELSNLEEDAWVQUDLHPRPGLSFRKYEMLKPHSQ	840
Qy	841	IPVSCBELPEESRLSRALSCNVSSPIFPAAGSVALLQMMFNTLVNNSWGDSEVELHANVTC	900
Dd	841	IPVSCBELPEESRLSRALSCNVSSPIFPAAGSVALLQMMFNTLVNNSWGDSEVELHANVTC	900
Qy	901	NNEEDSLLLEDSNATTIIPILYPINILIDQEDSTLYVSEFTPGRPKIHQVKHMYQVRIOPS	960
Dd	901	NNEEDSLLLEDSNATTIIPILYPINILIDQEDSTLYVSEFTPGRPKIHQVKHMYQVRIOPS	960
Qy	961	IHDHNIPTLEAVVGVPOPPSEBPTIHOMSVQMEPPYPCHYEDLERLPDAAPCLPGLALFR	1020
Dd	961	IHDHNIPTLEAVVGVPOPPSEBPTIHOMSVQMEPPYPCHYEDLERLPDAAPCLPGLALFR	1020
Qy	1021	CPVVRROELIVOVIGTLELVGRIEASSMPSLCSLSISFNSSKHFTLYGSNASTLAOVWK	1080
Dd	1021	CPVVRROELIVOVIGTLELVGRIEASSMPSLCSLSISFNSSKHFTLYGSNASTLAOVWK	1080
Qy	1081	VDVVVEKQMLYLYVLSGIGLLILLILFIVLYKVGFFKKNLEKMEAGRGVPPNGIPDAEDS	1140
Dd	1081	VDVVVEKQMLYLYVLSGIGLLILLILFIVLYKVGFFKKNLEKMEAGRGVPPNGIPDAEDS	1140
Qy	1141	EQLASGQAGADPGCLKPLHEKDSGSGGKD	1170
Dd	1141	EQLASGQAGADPGCLKPLHEKDSGSGGKD	1170
RESULT 13			
AA05782 standard; protein; 1170 AA.			
XX	AA05782;		
DT	25-MAR-2003	(revised)	
DT	09-JAN-2003	(revised)	
DT	23-AUG-1990	(first entry)	
XX			



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Db 601 VQAEQMTVLSSRPVVDVMTLMSFSPAEIPVHEVCSTSKMKRGVNTTICFOIKSLY 660
Qy 661 POFQGRVLANLTYTLQDGHRTTRRGLPGGRHRLRNIAVTTNSCTDFSFHPVQVD 720
Db 661 POFQGRVLANLTYTLQDGHRTTRRGLPGGRHRLRNIAVTTNSCTDFSFHPVQVD 720
Qy 721 LISPIVNSLNFSEEGTTPROQROQKDIPIILRSLHSEIWEIPEKNCCEKCCAN 780
Db 721 LISPIVNSLNFSEEGTTPROQROQKDIPIILRSLHSEIWEIPEKNCCEKCCAN 780
Qy 781 LRVSPSPSRRLRLTAFASSLSEVSLSLNEDEDAVWQDLPFGQLSPKRYEMLKPSQ 840
Db 781 LRVSPSPSRRLRLTAFASSLSEVSLSLNEDEDAVWQDLPFGQLSPKRYEMLKPSQ 840
Qy 841 IPVSCCELPBESRRLSRALSCVSSPIFKAGHVALQWMTLVNNSWGDVETLHANYTC 900
Db 841 IPVSCCELPBESRRLSRALSCVSSPIFKAGHVALQWMTLVNNSWGDVETLHANYTC 900
Qy 901 NNHBDLLLEDNSATITIPILYINILIDQEDSTLYVSTFPKPKIHQVKNMYQVRIQPS 960
Db 901 NNHBDLLLEDNSATITIPILYINILIDQEDSTLYVSTFPKPKIHQVKNMYQVRIQPS 960
Qy 961 IHDHNIPTLEAVVGVPPSPSEGIPTHMSVQMEPPVPCYEDLERLPDAEPCLPGLALFR 1020
Db 961 IHDHNIPTLEAVVGVPPSPSEGIPTHMSVQMEPPVPCYEDLERLPDAEPCLPGLALFR 1020
Qy 1021 CPVVRROELIVQVIGTLEIVGEIEASMSFSLCSSISIFNSKPHLYGSNLSLAQVVMK 1080
Db 1021 CPVVRROELIVQVIGTLEIVGEIEASMSFSLCSSISIFNSKPHLYGSNLSLAQVVMK 1080
Qy 1081 VDVIYERKQMLYLYVLSGIGGLLLILFIVLYKVGFPKRNILKXKMEAGRGVNGIPADS 1140
Db 1081 VDVIYERKQMLYLYVLSGIGGLLLILFIVLYKVGFPKRNILKXKMEAGRGVNGIPADS 1140
Qy 1141 EQLASGQAGDPGCCPKLHKDSESGGKD 1170
Db 1141 EQLASGQAGDPGCCPKLHKDSESGGKD 1170

RESULT 14
ADQ39423
ID ADQ39423 standard; protein; 1223 AA.
XX
AC ADQ39423;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1086.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-045135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin J, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
DR N-PEDB; ADQ38595.
XX

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PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1086; 145bp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1223 AA;
XX
Query Match 99.3%; Score 6061.5; DB 8; Length 1223;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 53; Gaps 1;
Qy 1 MKDSCITVMAMALLSGFFFPAPASSYNDVVGARSFSPRAGRHFGRVTVGVNGVYIGA 60
Db 1 MKDSCITVMAMALLSGFFFPAPASSYNDVVGARSFSPRAGRHFGRVTVGVNGVYIGA 60
Qy 61 PEGNSGTSLYQCCSGTGCHCLPVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Db 61 PEGNSGTSLYQCCSGTGCHCLPVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Qy 121 QNTYLSGLCYIFRONLQGPMLQGRPGFQECTKGNVDLVFLFDGSMISLOPDEFQKILDPMK 180
Db 121 QNTYLSGLCYIFRONLQGPMLQGRPGFQECTKGNVDLVFLFDGSMISLOPDEFQKILDPMK 180
Qy 181 DVMKKLSNTSYQFAAVQPSYKTEPSPDVYRKDDALLKHKVMULLNTGTGAINVY 240
Db 181 DVMKKLSNTSYQFAAVQPSYKTEPSPDVYRKDDALLKHKVMULLNTGTGAINVY 240
Qy 241 ATEVFRBELGARPDATVLIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESOETLH 300
Db 241 ATEVFRBELGARPDATVLIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESOETLH 300
Qy 301 KFAASKPASEFVKIIDTEBKLKDLFTBLQKIIYIEGTSKODLISFNNELSSGSIADLSR 360
Db 301 KFAASKPASEFVKIIDTEBKLKDLFTBLQKIIYIEGTSKODLISFNNELSSGSIADLSR 360
Qy 361 GHAVVAVGAKDWAAGFLLDKADLQDDPTIGNEPLFEVARGVLYGYVTWMLPSQKSTLL 420
Db 361 GHAVVAVGAKDWAAGFLLDKADLQDDPTIGNEPLFEVARGVLYGYVTWMLPSQKSTLL 420
Qy 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVQTHGTQISYFGELGCVVDVDDGETELLII 480
Db 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVQTHGTQISYFGELGCVVDVDDGETELLII 480
Qy 481 GAPLFYGEGRGGRVFIYQRRQLGRFBVSELOGDGRGYLGRRGELATLTLDINGGLVDVA 540

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Db      481  GAFIFYGQGRGVFIYORQOLGFEVEVELQDPDPIGRFGEATALTALDINGGLVDVA 540
Qy      541  VGAPLEBOGAYYIFNGRHGSLSPORSRIEGQVLSGIQWFGRSIHGKDLDEGDLAIVA 600
Db      541  VGAPLEBOGAYYIFNGRHGSLSPORSRIEGQVLSGIQWFGRSIHGKDLDEGDLAIVA 600
Qy      601  VGASQOMIVLSSRPVDMVTLMSPAPAI PVHEVBCSYSTSNKMGEGVNTITCPQISLY 660
Db      601  VGASQOMIVLSSRPVDMVTLMSPAPAI PVHEVBCSYSTSNKMGEGVNTITCPQISLY 660
Qy      661  POFQGRIVANITTYTQLDGHRTTRRGFLPGGRHHELRNIATVTSMSCTDSEFHPPVQD 720
Db      661  POFQGRIVANITTYTQLDGHRTTRRGFLPGGRHHELRNIATVTSMSCTDSEFHPPVQD 720
Qy      721  LISPIVNSLNSLWEEBGTPRDQROGKDIPILRPSLSHSEFWELPEKNGGDEKCCGAN 780
Db      721  LISPIVNSLNSLWEEBGTPRDQROGKDIPILRPSLSHSEFWELPEKNGGDEKCCGAN 780
Qy      781  LRVSPSPARBALRTAFASISVLSLSNLEDAWVQDLHPFGSLFRKVEMLKPHSQ 840
Db      781  LRVSPSPARBALRTAFASISVLSLSNLEDAWVQDLHPFGSLFRKVEMLKPHSQ 840
Qy      841  IPVSCBELPESRRLISRLSCNVSSPIFKAGHSVALQWMENTLYNSGSDVEIHLANTYC 900
Db      841  IPVSCBELPESRRLISRLSCNVSSPIFKAGHSVALQWMENTLYNSGSDVEIHLANTYC 900
Qy      901  NNEBSDLLIEDNSATTIPIIYPINILIDQEDSTLYSFTFKGPKIHQVKHMYQ----- 954
Db      901  NNEBSDLLIEDNSATTIPIIYPINILIDQEDSTLYSFTFKGPKIHQVKHMYQ----- 954
Qy      955  -----VRIPSIDHNIP 967
Db      961  EMQTSKQILICRPAGDAEHTVGAQEGELCPWGVSFAFRDNI RAGPCRVRIQPSIHDNIP 1020
Qy      968  TLEAVNGVPOPPSEGPITHQWSVQMEPPVPCHEYLELPLDAEPCLFGALFRCPVVRQ 1027
Db      1021  TLEAVNGVPOPPSEGPITHQWSVQMEPPVPCHEYLELPLDAEPCLFGALFRCPVVRQ 1080
Qy      1028  EILVOVIGTLELVGEIEASMFSLCSSLSISFNSKIHLYGSNLSAQVVMKVDVVEK 1087
Db      1081  EILVOVIGTLELVGEIEASMFSLCSSLSISFNSKIHLYGSNLSAQVVMKVDVVEK 1140
Qy      1088  QMLTYLVLSGIGLILLLIFIVLYKVGFPRKRLKEKMEAGRGVPGIIPADSEQLASGQ 1147
Db      1141  QMLTYLVLSGIGLILLLIFIVLYKVGFPRKRLKEKMEAGRGVPGIIPADSEQLASGQ 1200
Qy      1148  EAGDPGCLKPLHEKDSBSGGKD 1170
Db      1201  EAGDPGCLKPLHEKDSBSGGKD 1223

RESULT 15
ABU05070
ID      ABU05070 standard; protein, 1223 AA.
AC      ABU05070;
DT      29-JAN-2003 (first entry)
DE      Human expressed protein tag (EPT) #1736.
XX      Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW      protease; protease inhibitor; transporter; cytoskeletal protein;
KW      receptor; transcription factor; cancer; MHC;
KW      major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW      adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX      Homo sapiens.
XX      OS
XX      PN      WO000278524-A2.
XX      PD      10-OCT-2002.

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XX      28-MAR-2002; 2002WO-US009671.
PF      28-MAR-2001; 2001US-0279495P.
XX      21-MAY-2001; 2001US-0292544P.
PR      08-AUG-2001; 2001US-0310801P.
PR      01-OCT-2001; 2001US-0326370P.
PR      04-DEC-2001; 2001US-0336780P.
PR      20-FEB-2002; 2002US-0358985P.
XX      (Zyco-) ZYCOS INC.
PA      Chicx RM, Tomlinson AJ, Urban RG;
PI      WPI; 2003-040607/03.
XX      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT      leukemia.
XX      Example 2; SEQ ID NO 1736; 134pp; English.
PS      The invention describes a purified polypeptide, which comprises a
XX      fragment of a kinase, phosphatase, protease, protease inhibitor,
XX      transporter, cytoskeletal protein, receptor or transcription factor. The
XX      polypeptide is useful as an immunogenic composition for eliciting in a
XX      mammal an immunogenic response directed against any of the purified
XX      polypeptide. The purified polypeptide, or the antibody that binds to this
XX      polypeptide, is useful for treating cancer. The polypeptide is also
XX      useful for identifying compounds that binds to a naturally processed
XX      class I or class II MHC-binding polypeptide. The polypeptides and
XX      polynucleotides are particularly useful for treating or preventing
XX      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX      lymphoma or leukaemia. These are also useful for screening agents for
XX      treating the above mentioned diseases. This sequence represents an
XX      expressed protein tag (EPT) isolated from human tissue for translational
XX      profiling. Note: This sequence does not appear in the printed
XX      CC      specification but was obtained in electronic format directly from WIPO at
XX      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 1223 AA;
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Qy      Best Local Similarity 95.5%; Pred. No. 0;
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 30, 2005, 11:34:25 ; Search time 46 Seconds

(without alignments)  
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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## SUMMARIES

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## ALIGNMENTS

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US-08-789-078-2  
Sequence 2, Application US/08789078  
Patent No. 584385  
GENERAL INFORMATION:  
APPLICANT: Benedict, Stephen H.  
APPLICANT: Siahaan, Teruna  
APPLICANT: Chan, Marcia  
APPLICANT: Tibbetts, Scott  
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING  
TITLE OF INVENTION: IMMUNE TOLERANCE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: HOVEY, WILLIAMS, TIMMONS & COLLINS  
STREET: 1101 Walnut St.  
CITY: Kansas City  
STATE: MO  
COUNTRY: USA  
ZIP: 64106  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/789, 078  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/229, 513  
FILING DATE: 19-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26262  
REFERENCE/DOCKET NUMBER: 22833  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816)474-9050  
TELEFAX: 816/474-9057  
TELEX: 434-363  
INFORMATION FOR SBO ID NO: 2:  
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TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: T-cell  
CELL LINE: HL-60

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AUTHORS: Pigott,  
TITLE: LFA-1 Amino acid sequence (alpha) (from  
JOURNAL: PMA-stimulated HL-60 cells)  
PAGES: 94-95  
DATE: 1993  
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RESULT 2  
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 ; Patent No. 5863889

GENERAL INFORMATION:  
 APPLICANT: Benedict, Stephen H.  
 APPLICANT: Shahaan, Teruna  
 APPLICANT: Chan, Marcia  
 APPLICANT: Tibbets, Scott

TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING  
 IMMUNE TOLERANCE

TITLE OF INVENTION: IMMUNE TOLERANCE

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
 STREET: 1101 Walnut St.  
 CITY: Kansas City  
 STATE: MO  
 COUNTRY: USA  
 ZIP: 64106

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
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 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/752,633

FILING DATE:  
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
 NAME: Collins, John M.  
 REGISTRATION NUMBER: 26262  
 REFERENCE/DOCKET NUMBER: 22833

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (816)474-9050  
 TELEFAX: (816)474-9057  
 TELEX: 434-363

INFORMATION FOR SEQ ID NO: 2:  
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 ORGANISM: Homo sapiens  
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PUBLICATION INFORMATION:  
 AUTHORS: Pigott,  
 TITLE: LFA-1 Amino acid sequence (alpha) (from  
 TITLE: PMA-stimulated HL-60 cells)  
 JOURNAL: The Adhesion Molecule Facts Book  
 PAGES: 94-95  
 DATE: 1993

RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 1170  
 US-08-752-633-2

Query Match 99.9%; Score 6098; DB 2; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVWAMALLSGFFPPAPASSYNDVKGARSSPPRAGHFGYRLQVNGYIVGA 60  
 Db 1 MKDSCITVWAMALLSGFFPPAPASSYNDVKGARSSPPRAGHFGYRLQVNGYIVGA 60

Qy 61 PGRGNSGSLYOCQSGTGCLPTVLGNSNTSKYLGMTLATDPTDLSILACDGLSRTCD 120  
 Db 61 PGRGNSGSLYOCQSGTGCLPTVLGNSNTSKYLGMTLATDPTDLSILACDGLSRTCD 120

Qy 121 QNTYLSGLCYLFRONTQGPMLQGRPGFOBCIKGNVDLVFLFDGSMSLQDPDEFOKIIDFMK 180  
 Db 121 QNTYLSGLCYLFRONTQGPMLQGRPGFOBCIKGNVDLVFLFDGSMSLQDPDEFOKIIDFMK 180

Qy 181 DVNKKLSNTSYQPAVQFSTSYTEBFDSDYVRKQDPDALLKRVKMLLTNTFGAIIYV 240  
 Db 181 DVNKKLSNTSYQPAVQFSTSYTEBFDSDYVRKQDPDALLKRVKMLLTNTFGAIIYV 240

Qy 241 ATEVFRBEHIGARDPAKVLIIITDGEATDSGNDAKDIIRYIIGKHPQTESQETLH 300  
 Db 241 ATEVFRBEHIGARDPAKVLIIITDGEATDSGNDAKDIIRYIIGKHPQTESQETLH 300

Qy 301 KPASKPASRFVKLIDTFEKLKDLFTLQKKIYVIGSTSKQDLTSFNMELSSSGISADLSR 360  
 Db 301 KPASKPASRFVKLIDTFEKLKDLFTLQKKIYVIGSTSKQDLTSFNMELSSSGISADLSR 360

QY 361 GHAIVGAVGAKWAGFLDLKADLQDPTFIGNEPLEEVAGYLGTYVTWLPSPRQKTSLL 420  
DB 361 GHAIVGAVGAKWAGFLDLKADLQDPTFIGNEPLEEVAGYLGTYVTWLPSPRQKTSLL 420  
QY 421 ASAPRYOHNGRRLTQEPQGGHMSVOTIHGTQIGSVYRGELCGVDVNDDETELLI 480  
DB 421 ASAPRYOHNGRRLTQEPQGGHMSVOTIHGTQIGSVYRGELCGVDVNDDETELLI 480  
QY 481 GABLFYGEORGAVFIYQRRLQFEVEYSELQDPCGYLGRFGAITALTDINDGLADVA 540  
DB 481 GABLFYGEORGAVFIYQRRLQFEVEYSELQDPCGYLGRFGAITALTDINDGLADVA 540  
QY 541 VGAPLEBQAVYIENGHGLSPQSPRIGCTOVLSCIQMGFSGIHGVKLESDGLADVA 600  
DB 541 VGAPLEBQAVYIENGHGLSPQSPRIGCTOVLSCIQMGFSGIHGVKLESDGLADVA 600  
QY 601 VGASQMTVLSRPVDMTLMSPSPALIVHEVECSYTSNMKEGNTTICQKSLY 660  
DB 601 VGASQMTVLSRPVDMTLMSPSPALIVHEVECSYTSNMKEGNTTICQKSLY 660  
QY 661 POFQGRLVANLYTLQDGHRTTRRGILPFGRRHRLRNIAVTTSMSCDPSFHFPCVQD 720  
DB 661 POFQGRLVANLYTLQDGHRTTRRGILPFGRRHRLRNIAVTTSMSCDPSFHFPCVQD 720  
QY 721 LISPINVSINFSIMEBGTPRDPAQGDIPILRPSLHSETWEIPEKXCGEDKCEAN 780  
DB 721 LISPINVSINFSIMEBGTPRDPAQGDIPILRPSLHSETWEIPEKXCGEDKCEAN 780  
QY 781 LRVSPSPARARLRTPAFASLVELSLNLEBDAYWQDLHFPFGISFPRKVMLEKPHSQ 840  
DB 781 LRVSPSPARARLRTPAFASLVELSLNLEBDAYWQDLHFPFGISFPRKVMLEKPHSQ 840  
QY 841 IPVSCBEPRESRLSRALSCNVSPPIFKAGHSVALOMENTLVNSWGDVVELHANVTC 900  
DB 841 IPVSCBEPRESRLSRALSCNVSPPIFKAGHSVALOMENTLVNSWGDVVELHANVTC 900  
QY 901 NNBDSDLEBNSATTTIPIILYPINILIQDQEDSTLYVSTPKPKIHQVQMTQVRIOPS 960  
DB 901 NNBDSDLEBNSATTTIPIILYPINILIQDQEDSTLYVSTPKPKIHQVQMTQVRIOPS 960  
QY 961 IHNNIPTLEAVGVQPPSEGPITTHQMSVQMEBPVCHEDLERLPDAEPCLPGLFLR 1020  
DB 961 IHNNIPTLEAVGVQPPSEGPITTHQMSVQMEBPVCHEDLERLPDAEPCLPGLFLR 1020  
QY 1021 CPVFRQELIVQYIGTLELVGEIEASSMFLCSSLSISFNSSKHFLYGSNABLAQVVMK 1080  
DB 1021 CPVFRQELIVQYIGTLELVGEIEASSMFLCSSLSISFNSSKHFLYGSNABLAQVVMK 1080  
QY 1081 VDVYERKQMLYLYVLSGIGILLLLIFIVLYVGVFPKRMLEKMEAGRGVPGIPEADS 1140  
DB 1081 VDVYERKQMLYLYVLSGIGILLLLIFIVLYVGVFPKRMLEKMEAGRGVPGIPEADS 1140  
QY 1141 EQLASQGEADPGCLKRLHEKDSBSGGKD 1170  
DB 1141 EQLASQGEADPGCLKRLHEKDSBSGGKD 1170

RESULT 3  
PCT-US95-04886-2

Sequence 2, Application PC/TUS9504886  
GENERAL INFORMATION:  
APPLICANT: Benedict, Stephen H.  
APPLICANT: Sibaah, Teruna  
APPLICANT: Chan, Marcia  
APPLICANT: Tibbets, Scott  
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
STREET: 1101 Walnut St.  
CITY: Kansas City  
STATE: MO

COUNTRY: USA  
ZIP: 64106  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04886  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26262  
REFERENCE/DOCKET NUMBER: 22833  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816)474-9050  
TELEFAX: (816)474-9057  
TELEX: 434-363  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1170 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: T-cell  
CELL LINE: HL-60  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..25  
OTHER INFORMATION: /label= signal  
OTHER INFORMATION: /note= "Signal sequence"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 32..79  
OTHER INFORMATION: /label= Repeat  
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LOCATION: 339..391  
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NAME/KEY: Region  
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FEATURE:  
NAME/KEY: Domain  
LOCATION: 170..349

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OTHER INFORMATION: /label= IDomain
OTHER INFORMATION: /note= "I-Domain"
FEATURE:
NAME/KEY: Domain
LOCATION: 1089..1112
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OTHER INFORMATION: /note= "Transmembrane Domain"
FEATURE:
NAME/KEY: Domain
LOCATION: 1113..1170
OTHER INFORMATION: /label= Cyto
OTHER INFORMATION: /note= "Cytoplasmic domain"
PUBLICATION INFORMATION:
AUTHORS: Pigott,
TITLE: LFA-1 Amino acid sequence (alpha) (from
JOURNAL: The Adhesion Molecule Facts Book
PAGES: 94-95
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 1170
PCT-US95-0486-2

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Query Match          99.9%; Score 6098; DB 5; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MKDSCTVMAWALLSGFFFPAPASSYNLDVAGARSFSPPRGRHFGYVLYOVNGVTVGA 60
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DB 61 PGBENSTGSLYQCCSGTGCHLPTVLRGNSNTSKYLMTLATDPDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVPLFDGSMISLQDPFQKILDFMK 180
DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVPLFDGSMISLQDPFQKILDFMK 180
QY 181 DVMKGLSNTSYQFAAVQFSTSYKTEPFDSDYVKRDPDALIKVKNMLLTNTFGAINVY 240
DB 181 DVMKGLSNTSYQFAAVQFSTSYKTEPFDSDYVKRDPDALIKVKNMLLTNTFGAINVY 240
QY 241 ATEVFRELGARPATVYLIIITDGEATDSNDIAADIIRYIIIGIGKHQTKESQETLH 300
DB 241 ATEVFRELGARPATVYLIIITDGEATDSNDIAADIIRYIIIGIGKHQTKESQETLH 300
QY 301 KFAKSPASBEFKILDTPEKLDLFTLEOKKIYVEGTSKODLTSFNNELSSSGISADLSR 360
DB 301 KFAKSPASBEFKILDTPEKLDLFTLEOKKIYVEGTSKODLTSFNNELSSSGISADLSR 360
QY 361 GHAVVAGVAGAKDWAAGFLDLKADLQDDTFIGNEBLTPEVAGYLGYYTVMLPSPKQTSLL 420
DB 361 GHAVVAGVAGAKDWAAGFLDLKADLQDDTFIGNEBLTPEVAGYLGYYTVMLPSPKQTSLL 420
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DB 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVQIITGQISYFGEGLGVADVQDGETELLII 480
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DB 481 GAPLFYGEORGRVFIYORROLGFEERYSEIQGDPGYLGRFGELITLTLTINQGLADV 540
QY 541 VGAPLEBOGAVYIFNGRHGGLSPQSORIEGTQVLSGIQWFGRSIHGVKDLSEGLADVA 600
DB 541 VGAPLEBOGAVYIFNGRHGGLSPQSORIEGTQVLSGIQWFGRSIHGVKDLSEGLADVA 600
QY 601 VQASQMTVTSRPPVDMTILMSFPAEIPVHEVECSYSTSNMKEGVNTTICFOIKSLY 660
DB 601 VQASQMTVTSRPPVDMTILMSFPAEIPVHEVECSYSTSNMKEGVNTTICFOIKSLY 660
QY 661 POFQGRVAVNLTYTLQDGHRTTRRGFLPGGRHLEARNIAVTTSMSTDSFHPVVCQD 720
DB 661 POFQGRVAVNLTYTLQDGHRTTRRGFLPGGRHLEARNIAVTTSMSTDSFHPVVCQD 720

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DB 661 POFQGRVAVNLTYTLQDGHRTTRRGFLPGGRHLEARNIAVTTSMSTDSFHPVVCQD 720
QY 721 LISFINVSLNPSLMEEGTTPDQPAQCKDIPIPIRLPSLHSETWEIPERKCGEDKCEAN 780
DB 721 LISFINVSLNPSLMEEGTTPDQPAQCKDIPIPIRLPSLHSETWEIPERKCGEDKCEAN 780
QY 781 LRVSFSPARSRAIRLTAPASLVELSLSNLEDAVWQDLHPHPPGLSFPKQVETLKPSHQ 840
DB 781 LRVSFSPARSRAIRLTAPASLVELSLSNLEDAVWQDLHPHPPGLSFPKQVETLKPSHQ 840
QY 841 IVPSCBELPRESRLSRALSQNVSSPIFKAGSHVALQMENTLVNSWGDSEVLEHANVTC 900
DB 841 IVPSCBELPRESRLSRALSQNVSSPIFKAGSHVALQMENTLVNSWGDSEVLEHANVTC 900
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DB 1021 CPVVFROEILVOYIGTLELVGIEASMPFLCSLSISFNSKHFLYGSNASLAQVVMK 1080
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DB 1081 VDVIYERKQMLYLYLSGIGLLLLLIIFVLYKVGFEKRLKEMKEMAGVNPNGIPAEDS 1140
QY 1141 EQLASQGEADPGCLKPLHKKDSGSGKD 1170
DB 1141 EQLASQGEADPGCLKPLHKKDSGSGKD 1170

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RESULT 4
US-08-476-062A-42
Sequence 42, Application US/08476062A
Patent No. 5877275
GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1170 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-476-062A-42

Query Match 99.2%; Score 6058; DB 2; Length 1170;  
 Best Local Similarity 99.4%; Pred. No. 0;

Matches 1163; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 DB 1 MKDSCITVAMAMALISGFFFPAPASSYNLDVRGARSPFPRAHGFGRVLOVNGVYVGA 60  
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 DB 61 PGGNSTGSLYOCOSGTHCLPTLRGNTSKYLGMTLATDPTDGSILACDPLSRTCD 120  
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 DB 241 ATAVFREBELGARPDATVLIITIDGKATDSGNIDAADKIIIRYIIIGIKHPOTKESQETLH 300  
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 DB 481 GAFLFYGEORGRVFIYQRRQLGFEVSELQGPDPYLGFRGGAITALTIDINGDLVDA 540  
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 DB 541 VGAPLEQGAIVYIPNGRHGSLSPQSORIGSTQVLSGIQWFGSHYKVLBEGDLADVA 600  
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 DB 601 VGBESQWIVASRPVDMVTLMSPAPRIYVHEVEGYSYTNMKKEGWNITTCQIKSLY 660  
 QY 661 POFQGRLVANLYTLQDGHRTTRRGFLPGGRHLELRNINAVTSMSCITDPSFHPVQVD 720  
 DB 661 POFQGRLVANLYTLQDGHRTTRRGFLPGGRHLELRNINAVTSMSCITDPSFHPVQVD 720  
 QY 721 LIPIPIVSLNFSIMEEGTPRDQAGKDIPIIIRPSLHSETWEIPEKKGCEBKCEAN 780  
 DB 721 LIPIPIVSLNFSIMEEGTPRDQAGKDIPIIIRPSLHSETWEIPEKKGCEBKCEAN 780  
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 DB 781 LRVSPSPARARALRTFASISVELSLSNLEDAVWVQDLDHPPGSGSPKVEMLKXHSQ 840  
 QY 841 IPIVSCBELPESRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNNSWGDVVELHANVTC 900

DB 841 IPIVSCBELPESRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNNSWGDVVELHANVTC 900  
 QY 901 NNEDSDLEDNATATPIPLTPINILIOQDESTLYVSTPGPKTHQVKNYQVQIOPS 960  
 DB 901 NNEDSDLEDNATATPIPLTPINILIOQDESTLYVSTPGPKTHQVKNYQVQIOPS 960  
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 DB 1021 CPVFRQELIVQYIGTLELVGEIEASWFSLCSSLSISFNSSKHFTLYGSNLSAQVNMK 1080  
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 DB 1081 VDVYERKQMLYLYVLSIGLILLILIFLYLVKVGPFKNLLEKMGAGRVNGLPAEDS 1140  
 QY 1141 EQLASGEADPGCLKPLHEKXSESGGKD 1170  
 DB 1141 EQLASGEADPGCLKPLHEKXSESGGKD 1170

# RESULT 5 PCT-US96-01314-42

; Sequence 42, Application PC/TUS9601314

GENERAL INFORMATION:

APPLICANT: M. Amin Arnaut

TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or 555X

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/01314

FILING DATE: 30-JAN-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/380,167

FILING DATE: 30-JAN-95

ATTORNEY/AGENT INFORMATION:

NAME: John W. Freeman

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 00786/267001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 1170

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US96-01314-42

Query Match 99.2%; Score 6058; DB 5; Length 1170;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1163; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKDSCITVAMAMALISGFFFPAPASSYNLDVRGARSPFPRAHGFGRVLOVNGVYVGA 60  
 DB 1 MKDSCITVAMAMALISGFFFPAPASSYNLDVRGARSPFPRAHGFGRVLOVNGVYVGA 60

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 DB 61 PGEENSTGSLYQCCSGTGCHCLPVTLRGNSNTSKYLGMTLATDPTDGSLLACDPGLSRTCD 120  
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 DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGFQECIKGNVNDVFLFDGSMSLQPDFQKILDPFK 180  
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 DB 181 DVMKLSNTSYQFAAVQFSTSYKTEPSPDVYKRDPAKDKVHMLLNTGAINV 240  
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 DB 241 ATEVFEELGARPATVLLIITDGBATDSNDIAADIIIRYIIIGIGHPTKESQETLH 300  
 QY 301 KFASKPASEFVKILDTFEKLDLFTBLQKKIYIEGTSKODLTSFNNELSSSGISADLSR 360  
 DB 301 KFASKPASEFVKILDTFEKLDLFTBLQKKIYIEGTSKODLTSFNNELSSSGISADLSR 360  
 QY 361 GHAVVGAAGAKMAGFLDLKADLQDDTFIGNEBLTPREVAGYGYTVVMLPSRQKTSLL 420  
 DB 361 GHAVVGAAGAKMAGFLDLKADLQDDTFIGNEBLTPREVAGYGYTVVMLPSRQKTSLL 420  
 QY 421 ASGAPRYOHMGRVLLFQEPQCGHMSQVOTIHGQISYSGELCYDVNDQSTELLII 480  
 DB 421 ASGAPRYOHMGRVLLFQEPQCGHMSQVOTIHGQISYSGELCYDVNDQSTELLII 480  
 QY 481 GAPLFYGEORGRVFIYQRRQLGFEVSELOQDPGYLGRFGAIIYALTDINGGLDVA 540  
 DB 481 GAPLFYGEORGRVFIYQRRQLGFEVSELOQDPGYLGRFGAIIYALTDINGGLDVA 540  
 QY 541 VGAPLEBQAVYIFNGRHGSLSPQSQRIEQTQVLSGIQWFGRSIHGKDLBGGLDVA 600  
 DB 541 VGAPLEBQAVYIFNGRHGSLSPQSQRIEQTQVLSGIQWFGRSIHGKDLBGGLDVA 600  
 QY 601 VGASQMTIVSSRPVDMTLMSPSPAIPIVHEVSSYSTSNKKEVNTTICQIKSLY 660  
 DB 601 VGASQMTIVSSRPVDMTLMSPSPAIPIVHEVSSYSTSNKKEVNTTICQIKSLY 660  
 QY 661 POFQGRLVANLTYTLQDGHRTRRRGLPGGRHRLRNIAVTTSMSCDTSFHPVVCOD 720  
 DB 661 POFQGRLVANLTYTLQDGHRTRRRGLPGGRHRLRNIAVTTSMSCDTSFHPVVCOD 720  
 QY 721 LISPINVSLNFSIMEEGTFRDQRAQKDIPIILPRLSHSEWBIPEKXCGEDKCEAN 780  
 DB 721 LISPINVSLNFSIMEEGTFRDQRAQKDIPIILPRLSHSEWBIPEKXCGEDKCEAN 780  
 QY 781 LRVSPFASBARALRLTFAASLVELSLSNLEDAVYQDLHPPGCLSPKVEMLKHSQ 840  
 DB 781 LRVSPFASBARALRLTFAASLVELSLSNLEDAVYQDLHPPGCLSPKVEMLKHSQ 840  
 QY 841 IPVSCBELPRESRLSALSCNVSPIFKAGSHVALOMFNLTUNSSWGSVELHANVTC 900  
 DB 841 IPVSCBELPRESRLSALSCNVSPIFKAGSHVALOMFNLTUNSSWGSVELHANVTC 900  
 QY 901 NNEDSDLEJNDSATTTIPIILYPINILIQODEDSTLYVFTPKGKIHQVHMYQVRIOPS 960  
 DB 901 NNEDSDLEJNDSATTTIPIILYPINILIQODEDSTLYVFTPKGKIHQVHMYQVRIOPS 960  
 QY 961 IHDHNTFTLEAVGVPOPESEGPITTHQWSVQMEBPVCHYEDLERLDAAEPCLPGLFR 1020  
 DB 961 IHDHNTFTLEAVGVPOPESEGPITTHQWSVQMEBPVCHYEDLERLDAAEPCLPGLFR 1020  
 QY 1021 CPVVFROEIIYOVYIGTELVGEIEASSMFLCSLSLSPNSKXHFHLYGSANSLAQVVMK 1080  
 DB 1021 CPVVFROEIIYOVYIGTELVGEIEASSMFLCSLSLSPNSKXHFHLYGSANSLAQVVMK 1080  
 QY 1081 VDVVYERQMLYLYVLSGIGILLLLLIYLYKVFPRKMLKEMEAGRGVPGNIPAEBS 1140  
 DB 1081 VDVVYERQMLYLYVLSGIGILLLLLIYLYKVFPRKMLKEMEAGRGVPGNIPAEBS 1140

QY 1141 EQLASQGEADPGCLKPLHEKDSGGGKD 1170  
 DB 1141 EQLASQGEADPGCLKPLHEKDSGGGKD 1170  
 RESULT 6  
 US-08-630-172-9  
 : Sequence 9, Application US/08630172  
 : Patent No. 606054  
 : GENERAL INFORMATION:  
 : APPLICANT: Staerz, Uwe  
 : TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
 : TITLE OF INVENTION: LYMPHOCYTE VETO  
 : NUMBER OF SEQUENCES: 41  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Sheridan Ross & McIntosh  
 : STREET: 1700 Lincoln Street, 35th Floor  
 : CITY: Denver  
 : STATE: Colorado  
 : COUNTRY: U.S.  
 : ZIP: 80203  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Releasee #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/630,172  
 : FILING DATE:  
 : CLASSIFICATION: 514  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Cornell, Gary J.  
 : REGISTRATION NUMBER: 32,020  
 : REFERENCE/DOCKET NUMBER: 2879-36  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (303) 863-9700  
 : TELEFAX: (303) 863-0223  
 : INFORMATION FOR SEQ ID NO: 9:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1065 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-630-172-9  
 Query Match 90.6%; Score 5533.5; DB 3; Length 1065;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1061; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 26 YNIDVGARSFSPRRGRHFGYRVLYOVGNGVYVGAPEGNSGSLYQCCSGTGCHCLPVTL 85  
 DB 1 YNIDVGARSFSPRRGRHFGYRVLYOVGNGVYVGAPEGNSGSLYQCCSGTGCHCLPVTL 85  
 QY 86 RGSNTSKYLGMTLATDPTDGSLLACDPGLSRTCDQNTYLSGLCYLFRONTQGPMLQGRP 145  
 DB 61 RGSNTSKYLGMTLATDPTDGSLLACDPGLSRTCDQNTYLSGLCYLFRONTQGPMLQGRP 120  
 QY 146 GFQECIKGNVNDVFLFDGSMSLQPDFQKILDPKDMVKKLSNTSYQFAAVQFSTSYKTE 205  
 DB 121 GFQECIKGNVNDVFLFDGSMSLQPDFQKILDPKDMVKKLSNTSYQFAAVQFSTSYKTE 180  
 QY 206 FPDFSDYKRDPAKDKVHMLLNTGAINVYATEVFEELGARPDATKVLIIITDG 265  
 DB 181 FPDFSDYKRDPAKDKVHMLLNTGAINVYATEVFEELGARPDATKVLIIITDG 240  
 QY 266 EARDSDNIDAADIIIRYIIIGIGHPTKESQETLHFAKPSAEFVKILDTFEKLDLFT 325  
 DB 241 EARDSDNIDAADIIIRYIIIGIGHPTKESQETLHFAKPSAEFVKILDTFEKLDLFT 300  
 QY 326 ELQKKIYIEGTSKODLTSFNNELSSSGISADLSRGAHVAVGAGADWAGFLDLKADIQ 385  
 DB 301 ELQKKIYIEGTSKODLTSFNNELSSSGISADLSRGAHVAVGAGADWAGFLDLKADIQ 360

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QY 386 DDTFIGNEPITPEVRAGYLGVTWTLPSROKTSILASGAPRYOHMGRVLLFOEPGGGHW 445
D 361 DDTFIGNEPITPEVRAGYLGVTWTLPSROKTSILASGAPRYOHMGRVLLFOEPGGGHW 420
QY 446 SQVQTHGTQIGSYFGGELCGVDVDDGETE-LILIGAPLYGBOGRGVFIYORQLGF 504
D 421 SQVQTHGTQIGSYFGGELCGVDVDDGETE-LILIGAPLYGBOGRGVFIYORQLGF 480
QY 505 EEVSEIQQDGYPLRGGEALITLTDINGDLVDVANGAPLEBQAVYIFNGRHGGLSPQ 564
D 481 EEVSEIQQDGYPLRGGEALITLTDINGDLVDVANGAPLEBQAVYIFNGRHGGLSPQ 540
QY 565 PSORIBGTQVLSGIQWFGRSIHGKDLBGLADVANGAESOMIVLSRPVDMVTLSMF 624
D 541 PSORIBGTQVLSGIQWFGRSIHGKDLBGLADVANGAESOMIVLSRPVDMVTLSMF 600
QY 625 SPAEIPVHEVCYSTSNKKEGVNITICFOIKSLYPOGRLVANTYTLQLDGHRTTR 684
D 601 SPAEIPVHEVCYSTSNKKEGVNITICFOIKSLYPOGRLVANTYTLQLDGHRTTR 660
QY 685 RGLFPGGRHRLRNIAVTTSMCTDPSFHPVVCVODLISPINVSINLSMBEETPRDOR 744
D 661 RGLFPGGRHRLRNIAVTTSMCTDPSFHPVVCVODLISPINVSINLSMBEETPRDOR 720
QY 745 AOGKDIPIILRPSLHSETWEIPEKNCGBDKCCBANLRVSFSPARSALRLTAFAISLVE 804
D 721 AOGKDIPIILRPSLHSETWEIPEKNCGBDKCCBANLRVSFSPARSALRLTAFAISLVE 780
QY 805 LLSLSNEEDAYWQDLHPPPGSLFRKVEMLKPHSQIPVSCBELPEESRLISRALSCNVS 864
D 781 LLSLSNEEDAYWQDLHPPPGSLFRKVEMLKPHSQIPVSCBELPEESRLISRALSCNVS 840
QY 865 SPIFKASHVALQMNEMTLVNSWGDVVELHANTCNNEEDSLLEDSATLPIILYPIN 924
D 841 SPIFKASHVALQMNEMTLVNSWGDVVELHANTCNNEEDSLLEDSATLPIILYPIN 900
QY 925 ILIQQDQDSTLYSFTFKGPKIHQVKNYQVRIOPSIDHNIPTLEAVGVPOPPSEGP 984
D 901 ILIQQDQDSTLYSFTFKGPKIHQVKNYQVRIOPSIDHNIPTLEAVGVPOPPSEGP 960
QY 985 THQMSVQMBEPVPCHEYDLERLPDAEPCLPGALFRCPVVRROELIVQITLVEIE 1044
D 961 THQMSVQMBEPVPCHEYDLERLPDAEPCLPGALFRCPVVRROELIVQITLVEIE 1020
QY 1045 ASSMFSICSSLSISFNSSKPHLYGSNASTLAQVVMKVDVYEEKM 1089
D 1021 ASSMFSICSSLSISFNSSKPHLYGSNASTLAQVVMKVDVYEEKM 1065

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RESULT 7
US-09-375-419-9
; Sequence 9, Application US/09375419
; Patent No. 6264950
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,419
; FILING DATE:
;

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-375-419-9
Query Match 90.6%; Score 5533.5; DB 3; Length 1065;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1061; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 26 YNLDVGAASFSPPRAGRHGYRVLYQVANGVIYGAEGNGSTSLYQCOSGTGHCUPVTL 85
D 1 YNLDVGAASFSPPRAGRHGYRVLYQVANGVIYGAEGNGSTSLYQCOSGTGHCUPVTL 60
QY 86 RGSNTYSKYLGMTLADPTDGSILACDPSLSRCDONTYLSGLCYLFRONLQSPMLQGRP 145
D 61 RGSNTYSKYLGMTLADPTDGSILACDPSLSRCDONTYLSGLCYLFRONLQSPMLQGRP 120
QY 146 GFQECIKGNVDLVELPDGSMLOPDEFOKILDPKQVMKKLSNTSYOPAVOPSTSYKTE 205
D 121 GFQECIKGNVDLVELPDGSMLOPDEFOKILDPKQVMKKLSNTSYOPAVOPSTSYKTE 180
QY 206 FDFSDYVKRDPDALLKHYKMLLTNTFGAINVYAVEVREELGARPDATKYLIIITDG 265
D 181 FDFSDYVKRDPDALLKHYKMLLTNTFGAINVYAVEVREELGARPDATKYLIIITDG 240
QY 266 EATDSGNIDAADKIITYIIGIGHFQTKESQETLHFAKSPASEPKIITDFEKLDT 325
D 241 EATDSGNIDAADKIITYIIGIGHFQTKESQETLHFAKSPASEPKIITDFEKLDT 300
QY 326 ELQKTIYVIGTSGKQDLSFNNELSSSGISADLSRGHVVGAAGVADWAGFDLKAQD 385
D 301 ELQKTIYVIGTSGKQDLSFNNELSSSGISADLSRGHVVGAAGVADWAGFDLKAQD 360
QY 386 DDTFIGNEPITPEVRAGYLGVTWTLPSROKTSILASGAPRYOHMGRVLLFOEPGGGHW 445
D 361 DDTFIGNEPITPEVRAGYLGVTWTLPSROKTSILASGAPRYOHMGRVLLFOEPGGGHW 420
QY 446 SQVQTHGTQIGSYFGGELCGVDVDDGETE-LILIGAPLYGBOGRGVFIYORQLGF 504
D 421 SQVQTHGTQIGSYFGGELCGVDVDDGETE-LILIGAPLYGBOGRGVFIYORQLGF 480
QY 505 EEVSEIQQDGYPLRGGEALITLTDINGDLVDVANGAPLEBQAVYIFNGRHGGLSPQ 564
D 481 EEVSEIQQDGYPLRGGEALITLTDINGDLVDVANGAPLEBQAVYIFNGRHGGLSPQ 540
QY 565 PSORIBGTQVLSGIQWFGRSIHGKDLBGLADVANGAESOMIVLSRPVDMVTLSMF 624
D 541 PSORIBGTQVLSGIQWFGRSIHGKDLBGLADVANGAESOMIVLSRPVDMVTLSMF 600
QY 625 SPAEIPVHEVCYSTSNKKEGVNITICFOIKSLYPOGRLVANTYTLQLDGHRTTR 684
D 601 SPAEIPVHEVCYSTSNKKEGVNITICFOIKSLYPOGRLVANTYTLQLDGHRTTR 660
QY 685 RGLFPGGRHRLRNIAVTTSMCTDPSFHPVVCVODLISPINVSINLSMBEETPRDOR 744
D 661 RGLFPGGRHRLRNIAVTTSMCTDPSFHPVVCVODLISPINVSINLSMBEETPRDOR 720
QY 745 AOGKDIPIILRPSLHSETWEIPEKNCGBDKCCBANLRVSFSPARSALRLTAFAISLVE 804

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Db 721 AAGKDIPILRPSLHSETWEIFEKNCGEDKCEANLRVSPSPARSRLRLTAFASLSVE 780  
 Qy 805 LLSLNEEDAYWOLDLHFPGLSPKRYEMLKPHSOIPVSCBEPESRLLSRALSCNVS 864  
 Db 781 LLSLNEEDAYWOLDLHFPGLSPKRYEMLKPHSOIPVSCBEPESRLLSRALSCNVS 840  
 Qy 865 SPIKAGSHVALQWMPNTLVNSMGDSVELHANVTCCNEDSDLEJNSATTIIPILPIN 924  
 Db 841 SPIKAGSHVALQWMPNTLVNSMGDSVELHANVTCCNEDSDLEJNSATTIIPILPIN 900  
 Qy 925 ILIQDQDSTLYVSTPKGPKIHQVKMYQVRIOPSIDHNIPTLEAVGVGPQPSGPI 984  
 Db 901 ILIQDQDSTLYVSTPKGPKIHQVKMYQVRIOPSIDHNIPTLEAVGVGPQPSGPI 960  
 Qy 985 THQMSVQMPVPVPHYEDLELTPDAAPCFGLFRCPPVFRQILVQVIGTLELVEIE 1044  
 Db 961 THQMSVQMPVPVPHYEDLELTPDAAPCFGLFRCPPVFRQILVQVIGTLELVEIE 1020  
 Qy 1045 ASSWESLCSLSISFNSSKPHFLYGSNLSLAQVVMKVQVVEKQK 1089  
 Db 1021 ASSWESLCSLSISFNSSKPHFLYGSNLSLAQVVMKVQVVEKQK 1065

## RESULT 8

US-08-173-497-3  
 : Sequence 3, Application US/08173497  
 : Patent No. 5437958  
 : GENERAL INFORMATION:  
 : APPLICANT: Gallatin, W. Michael  
 : APPLICANT: Van Der Vliet, Monica  
 : TITLE OF INVENTION: No. 5437958e1 Human 2 Integrin Alpha  
 : NUMBER OF SEQUENCES: 29  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 : STREET: 233 S. Wacker Drive, 6300 Sears Tower  
 : City: Chicago  
 : STATE: Illinois  
 : COUNTRY: USA  
 : ZIP: 60606-6402  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: IBM PC compatible  
 : SOFTWARE: Patent Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/173,497  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: No. 5437958and, Greta E.  
 : REGISTRATION NUMBER: 35,302  
 : REFERENCE/DOCKET NUMBER: 27866/31363  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 312-474-6300  
 : TELEFAX: 312-474-0448  
 : TELEX: 25-3856  
 : INFORMATION FOR SEQ ID NO: 3:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1153 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-173-497-3

Query Match 25.6%; Score 1563; DB 1; Length 1153;  
 Best Local Similarity 34.3%; Pred. No. 1.9e-124;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;  
 Qy 6 ITWAMALLSGFFFPADASSYNDLVGRSPSPRAGRHGYRVLQV-GNGVIVGAGE- 63  
 Db 6 LILTALTLCHGF-----NLDTENAMTFQ--ENARGFGQSVVQLOGSRVVGAFQEI 54

Qy 64 --GNSGTSLYQCGSGTGHCLPVLIR-GSNTYSKYLGTATLTPDGSIIACDPGLSTCD 120  
 Db 55 VAANQSGSLYQCYSTSGSCPIRLQVPEAVNMSLGLSLAATTSPPQLACGPIVHQTCS 114  
 Qy 121 QNTYLSGLCYLFPQNLQGLPGLQGRPGFQECIKG---NVDLVFIPDSMSLQDPEFOKIT 176  
 Db 115 ENTVYKLCFLFGSNLR---QDPQKFEALRQCPQEDSIATLIDSGSIIIPDFRMRK 170  
 Qy 177 DPMKDVKKLSNTSYQPAVQFSTYKTEPDSYVYRKPDDALKHVKMLLTNTFGA 236  
 Db 171 EFWSTVWQLKSKSLTFLSLQYSEEFRIHFTFKEPQNNPFRSLVKRITQLGRTHTATG 230  
 Qy 237 INVATVPEBEIAGAPDARKVLIIITDGR--ATDSNDIAAD----IIRYIIIGKX 289  
 Db 231 IRKVRRELFTITGARNAKRLIVITDGBKFDPPDLYEYVIEPADREGIIRYVIGVDA 290  
 Qy 290 FQTKESQETLHKASKPSEFVKILDTPEKLDLFTLEOKIYIEGTSKODLTSFMMEL 349  
 Db 291 FRESKQELNTLASKPRPDHVQVNNFELKTIQNLREKIRAIETGTQSGSSFEHEM 350  
 Qy 350 SSGISADLSRGAHVAGVAKDMAGGFLDKADLDDPTFIGNEPITPEVRAGYLYTVT 409  
 Db 351 SQSGFSAITSNGPBLSTVGSYDMAGVF-LYTSKEKSTINMTRVDSNNDAVLYGAAA 409  
 Qy 410 WLPDRQKTSILASGAPRYQMGKVLFPQEQGGHMSQVOTINGTOIGSTFGELGVDV 469  
 Db 410 -ILIRNVOSLVVIGAPRYOHIGLVAMFR--QNTGMESNANVGTQIGAYFGASLCSDV 466  
 Qy 470 DQGETELLIGAPLFPGBGGRGVFIY-----ORQLGFEVSELOGDGYLGRGEA 524  
 Db 467 DSGSTDLVIGAPHYEEQTRGVQVSCPLPRQQRAMQCDAY--LYGEGQGPWGRGAA 524  
 Qy 525 ITALTIDNGDLVAVAGAPLEB--OGAVYIFNGRHG-GLSPQSPQRIEQTQVLSGIQWF 581  
 Db 525 LTVLGVDNGKLDVAIGAGEEDNRGAVLFTGTSGSGISPSHSQRIASKXSLPRQYF 584  
 Qy 582 GRSIHGVKIDEGDLADVAGASQMIVLSRPVDMVTLMSPSPAIPIPHEVCSYSTS 641  
 Db 585 QGSLGGQDLTMGLVDLTVGAQGHVLLRSQVLKALMEFNPBEVANVEPCNDQV 644  
 Qy 642 NKKEGNITICQI-KSLYPOF-QGRIVANLTYTQLDCHRRRRLGFPQGHLELRNI 699  
 Db 645 -KKEKEGVAVCLHVKSTDRLEBQISGVVYDIALSGRSHRAVFEYNKSTRQT 703  
 Qy 700 AYT-TSMSCDTDFSFHPVQVDLISPINVSINSLWEEBETPPDQRAQKDIPILRPSL 758  
 Db 704 QVGLGYTCETLKLQPLNCIEDVPSPILVRLNFSL---VGTPLS-AFGN-----LRPV 753  
 Qy 759 HSETWEI----PFRNCGEDKCEANLRVSPSPARSRLRLTAFASLSVELSLNEED 813  
 Db 754 ABDAQRLFTALPFEKNCGNDNICODDLSTTFMSLDCLVGGPREFNTVTVRNDGED 813  
 Qy 814 AYVAVOLDHFRPGLSRKRYEML---KPHSOIPVSCBEPESRLLSRAL---SCNVSPI 867  
 Db 814 SYRTQVTFPPPLDLSYRKVSTLONORSORSWRLACES--ASTVEVGALKSTCSINHPI 871  
 Qy 868 FKAGSHVALQWMPNTLVNSMGDSVELHANVTCCNEDSDLEJNSATTI---IPIIYPIN 924  
 Db 872 FPNSEVTNITITVDVSKASLGNKLLKANVTSENN---MPTNKTETPELPPVKAAY 927  
 Qy 925 ILIQDQDSTLYVSTPKGPKIHQVKMYQVRIOPSIDHNIPTLEAVGVGPQPSGPI 984  
 Db 928 MVTLSHGVSFTKYNLFTASEVTSRVMQHOQV---SNLQGSRLP-ISLVFLVPLRLQTVI 983  
 Qy 985 THQMSVQMPVPV--PHYEDLELTPDAAPCFGLFRCPPV-----1024  
 Db 984 WDRPQVTFSENLSTCHTK--ERLPESHSD--FLAEIRKAPVAVNCSTAVCCIOCDIPFPG 1039  
 Qy 1025 FROEIIYQVIGTLELVEIEAS-SMFSLCSLSISFNSSKPHFLYGSNLSLAQVVMKVQ 1082  
 Db 1040 IQREPNATLKNISFPWYIKTSHNHLIYSTAIIILFNDVSFTLLPQGAFAVRSQTETKVR 1099





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STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-3
Query Match 25.6%; Score 1563; DB 1; Length 1153;
Best Local Similarity 34.3%; Pred. No. 1,9e-124;
Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;
QY 6 ITTAMALLSGFFFPASSYINDVGARSPSPRAGRHFGRVLYQV-GNGVIVGABGE- 63
DB 6 LLLTALLTLCGIF-----NLDTENAMTFQ--ENARGQSVVQLQSGRVVVGARQEI 54
QY 64 --GNSSTSLVQCCSGTGHCLPVYLR-GSNTSKYLGKTLATDPDGSILACDPGLSTCTD 120
DB 55 VAAQQRSLVQCDYSTGSCBETIRLQVVEAVNMSLGSLAATYSPQLLACGPTVHQTCS 114
QY 121 QNTYLSGLCYLFRONLQGRPMLOGRPFQFCIKG---NVDLVPLFDGSMSLQDEFOKITL 176
DB 115 ENTIVKGLCFLFGSNLR-----QDPQKPEALRGCPQSDIAFLIDSSGIIPHDFRMMK 170
QY 177 DPMKDVWKLSNTSYQPAVQFSTYKTEBFDSDYVRKQPDALLKHKMLLTNTFGA 236
DB 171 EFTSVWEOKKSKTFLPSLMQYSEPRHIFTFKFKQNNPNRSLVKRTYQLDGLGTHATG 230
QY 237 INVATVFEELGARGDATKVLIIITDGE--ATDSGNIDAAD-----IIRYIGIGK 289
DB 231 IRRVRLRFLNITGARGAKRKLIVITDGEKFGDPLGYEVNIPBADREGVIRVYIGVDA 290
QY 290 FQTKESQETLHKFASRPFVKLIDTFEKLKDLFTLEOKKIYITEGSKQDLTSPMEL 349
DB 291 FRBKSKQBLNTLASKPRPDHVPQVNNFPAKTIQMDLREKIPAISETGSSSSFEHEM 350
QY 350 SSSGISADLSRGAAVAVGAKDWAGFLDLKADLQDDTIGNEPLTPVRAAGLYGYVT 409
DB 351 SOEGFSAITSNGFLSTVGSYDWAQGVF-LYTSKSKSTFINMTRVDSMDMDAIVGYAAA 409
QY 410 WLSRQKTSLSLASGARPYQMGVRLRLQDFQGGGSHMSQVQTIHOTIGSFGGELCGVDV 469

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DB 410 -ILLRNRVQSLVAGAPRYQHILGAVMR--QNTGMESNANVGTQIGAFGSLGCVDV 466
QY 470 DQGETELLIGAPLFPGEQGRGVLY-----QRQLGFEBSYSELODGYPLGRGEA 524
DB 467 DSGSTDLVLIGAPHYEQTRGGQVSCPLPRGQARMQCDAY--LYGEOQGPWGRGAA 524
QY 525 ITLTLTIDNSGVLVDVAVGAPLRE--OGAVYIFNGRHG-GISPDQSORIESTOVLISGLOWF 581
DB 525 LTVLGDVNGSKLTDVALGAPGEEDNRGAVLFGHTSSGSISSHSQIASKSLSPRLQYF 584
QY 582 GRSIHGVKLEGGDLADVAAGASOMIVLSSRPVDMVATLMSFSPAPRIVHVECSYSTS 641
DB 585 GQSLSGGQDLTMNGVLDLTVGAQGHVLLASQVYLRKAKALMENPRVAVANVEFCNDQV 644
QY 642 NKKEGVNITICFOI-KSLVPQF-QGRLVANLTYTTLQDGHRTTRRGLPFGGRHELRNI 699
DB 645 -KKEAGEVAVCLHVGQSTRDLREGQIQSVVYTDLALDGRPHSRVAFVNETKSTRQT 703
QY 700 AVT-TSMSCIDPSFHPVVCYQDLISPIVNSLMSBEGTPRQRAQGDIPILRPSL 758
DB 704 QVIGLTQTCETLKLQLENCIEDPVSPIVLRNLPSL--VGTPLS--AFGN-----LRPVL 753
QY 759 HSETWEI-----PPEKNCGEDKCEANLAVSFSPARSRALRLTAFASLYELSLNLEED 813
DB 754 AEDAQRLFTLFPPEKNCQNDNICQDDLSTFSPMSLDCIVGGRPREFNVTVYRANGED 813
QY 814 AYVWQDLHPPPGLSFRKVEML--KPHSQIPVSCBELPESRLLSRAL--SCNVSSPI 867
DB 814 SYRTQVTFPPPLDLSTRKAVSTLQNSQSRQSMRLACBS--ASTREVSQALSTSCSIHPI 871
QY 868 FKAGSHVALQMMNTLVNSGSDSVELHNAVYTCNEDSLLEDSATTT--IPILYPI 924
DB 872 FPNSEVTFNITPDVSKASLGNKLLKANVTSENN---MPTNKTEFQLEIPVKAAY 927
QY 925 ILIODEDSTLYVSTFKPGPKIHQVKMYQVRLQPSIHNDHNPITLAVAVGVPQPSRGP 984
DB 928 NVVTSHGVSXTKYNLFTASNTSRVMQHOYQV---SNIGQSLP-ISLVPLVPRLNQTVI 983
QY 985 THQMSVQMBPPV--PCHYDLRLPLDAEPCLPALFRCPV----- 1024
DB 984 WDRPQVTFSENLSSTGHTK--ERLPSHD--FLAEKRAKVAVNCISIAVQRICODIPFG 1039
QY 1025 FROELVQVIGTLELYGEIRAS-SMFSLSSLSISFNSSGHFHLYGNSAL-AQVVMKV 1082
DB 1040 IOEFNAATLKGNSLSPWYIKTISHNHLIVSTAILFNDSTVFTLLPGGAGARVSCOTERKE 1099
QY 1083 VVVEKQMLYLYVSGIGLILLIIFLYLYKQVFPFRNKKERKEAGRGVNGIP 1136
DB 1100 PFEVNPPLVIVGSSVGGILLLITLALYKGLFPRQYKDMSEG-GPYGAB 1152
RESULT 11
US-08-362-652-3
Sequence 3, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vliet, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-3

```

```

Query Match      25.6%; Score 1563; DB 1; Length 1153;
Best Local Similarity 34.3%; Pred. No. 1,9e-124;
Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

QY 6 ITWAMALISGFEPFAPASYNLDVVGARSPPRAGRGVYLVY-GNGVVGAGE- 63
DB 6 ILLTALTLGCF-----NDTENAMTFQ--ENARGFQSVVLQSRVAVGAPQEI 54
QY 64 --GNSTGSLVQCGSTGCHLPVTLR--GSNYTSKYLQMTLATDPTDGSILA 120
DB 55 VANQSGSLVQCYSTGSCSPRIRLQVVEAVNMSISGLSLAATTSPPQLACGPTV 114
QY 121 QNTYISGLCTLPFQNLQGPMLQGRPGQECIKG---NDVLVLPFDGSMLODERQKIL 176
DB 115 ENTYVGLGCLFGLFSNLR---QOPQKPEALRGCPQSDSIALVLDSSGSIIPHDFRMK 170
QY 177 DFKMDVKKLSNYSYQPAVQFSTYKTEPFDSDYVARKPDALLKHKVMMLLTNTFGA 236
DB 171 EFTSTMEQKSKTLPFLMJOYSEBRRIHTEKQFNPNPRLVAPRTDGLRTHRTATG 230
QY 237 INVATEVFEELGARDATKVLIIITDGE--ATDSGNIDAND-----IIRYIIGIKH 289
DB 231 IRVAVLEFNIITGARKNAFKILVITDSEKFGDPLGYEDVIEADREGVIRYVIGDA 290
QY 290 FQTKSQEOTLHAKASRPASFVKILDTFEKLDLFTLEOKKIYIESTSKODLSTFMEL 349
DB 291 FSEKSRQELNTLTAKPRPDHVPQVNNFELKTIQNLREKIRAIETQVSSSSFEHEM 350
QY 350 SSSGISADISRGHAVVGAVKAMAGGFLDKXDLDDFTIGNEBPLPEVRAGLGYTVT 409
DB 351 SQEGFSAITSNQPLSTVSGSYMAGGV--LYTSKESSTIINNTRVSDMNDAYLGYAAA 409
QY 410 MLPSPQKTSLLASGAPRYQHMGRVLLFQEPQGGHMSQVOTIQTQIGSYFGEGLGCV 469
DB 410 -ILRRRVGSLVAGAPRYQHIGLVAMFR--QNTGMESNANVSGTOIGAFGASLGV 466
QY 470 DQDGETELLIGAPLFYGEQRCGRVFTY-----QRQLGEBEVSSELOGDPYGLRGE 524
DB 467 DSNQSTDLVIGAPHYEQRGGQVSVCPPLPRQGRAMQCDAY--LYGEOGQPWGRGAA 524
QY 525 ITALTINNGGLVDVAVGAPLEB--OGAVYIENGRRHG--GLSPQSPQRIEKGTVLSGIOM 581
DB 525 LITVLDVNGDKLTDVAIGAPGEBDNKGAIVLFGHTSGSGISPSHSQKSLASGSPRLQY 584
QY 582 GRSIHGVKDLGGDGLDVAVGASOMLVLSRPVDMVTLMSPSPAIPIVHEVCSYSTS 641

```

```

DB 585 GOSLGGQDLTMDGLVDLTVGAQGHVLLRSQPLVRKVAIMEFNPREVARNVECDQVY 644
QY 642 NMKEGVNITICQOI--KSLYPQF--QGRIVANLTLYTLQDGHTRRRGLPGGRHLEARRVI 699
DB 645 -KKEAGEVRCVLHQAQSTRDLRBLRQIQSVVTVYDALDSGRPHSAVNETKSTRKOT 703
QY 700 AVT--TSMSCDPSFHPVPCVDLISPINVSINFSIMEBGRTPRQAOQKDIPIILRPSL 758
DB 704 QVLGLQTCETLKLQPLNCIEDPVSPIVLRNPSL---VGTLS--AFGN-----LRPVL 753
QY 759 HSETBEI-----PRENCGEDKKCEANLRVSSPARSRLRLTAPASLSVEISLSEED 813
DB 754 AEDAQRLFTLALPFPFKNCNDINIQQDDLSITFSFMSIDCLVYGPREFVTVYVRNDGD 813
QY 814 AYWVOLDLHPPGLSRKXEML---KPSQIVSCGELPEESRLLSRAL---SCNVSPPI 867
DB 814 SYRTQVTFPPLDLSTRKVTIQQNQSQSRMLACES--ASTEVSGALKSTSCINHP 871
QY 868 FKAGHSVALQMMFNTLVNSMGDSVELHANVTCONNEDSLLBEDNSATTI---IPILYPTN 924
DB 872 FPENSEVTNITFDVDSKASLGNKLLKANVISENN---MRTNKTETQLELPVYAVY 927
QY 925 ILIQDQEDSTLYSFTPKPKTHQVKMYQVRIQPSIHDMNITPLEAVVGVPOPEBEGPI 984
DB 928 MVTSHGVSTKYLINFASENTSRVMQHOYQV---SMLAGORSLP--ISLVELVPVRLNQTVI 983
QY 985 THQMSVQMPPV--PCYVEDLERLPPDAEPCPLGALFRCPPV----- 1024
DB 984 WDPQVTFEENISSTHTX--ERLPESHDP--FLAEIRKAPVNVCSIAVQRIQCDIPFG 1039
QY 1025 FROELIVQVIGTLELVGEIENS--SMFSLCSLSISFNSKPHLYGSNASL--AQVVMKYD 1082
DB 1040 IQEENFATLKNLSFPMWYIKTSHNHLIVSTAEILFNDSVFILLPQGAFAVSQETKYE 1099
QY 1083 VYEEKOMLYLVLSGIGLLLLILFTVLYKVGFFRRNILEKQMEAGRVPNQIP 1136
DB 1100 PFEVNPRLPLIVGSSVGGILLLALITPAALYKLGFFKRYQKDMMSSEG--GPQAP 1152

RESULT 12
US-08-605-672-3
Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: Van der Vlieten, Monica
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994

```

ATTORNEY/AGENT INFORMATION:  
 NAME: Williams Jr., Joseph A.  
 REGISTRATION NUMBER: 38,659  
 REFERENCE/DOCKET NUMBER: 27866/32684  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1153 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-605-672-3

Query Match 25.6%; Score 1563; DB 2; Length 1153;  
 Best Local Similarity 34.3%; Pred. No. 1,9e-124;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

```

QY 6 ITWMAALLSGPPFPADASSYNDVGRASFPSPRAGHFGYRLVQV-GNGVIVGAPGE-63
DB 6 LILTLATLCHGF-----NLDTENAMTFQ--ENARFGQGVVQLQSGRVVVGAFQEI 54
QY 64 --GNSGTSLVQCOSGTHCLPVTLR-GSNTSKYLGHTLATDPDGSILACDGLSKTCD 120
DB 55 VAANQRSLVQCYSVSGSCPEIRLQVPEAVNMMSLGLSLATATSPQLLACGFLVHTQS 114
QY 121 QNTYLSGLCYLFRONLOGPMLQGRPGFOECIKG---NVDLVFLFDGSMLOPDEPOKIL 176
DB 115 ENTYYKGLCELFSGSNLR---QDPQKPEALRGCPQEDSIALILDSGSIIPHDFRKM 170
QY 177 DFKMDVKKLSNTSYOPAAVOFTSYKTEPDSYVVRKDPDALLKHKMLLTYTPGA 236
DB 171 EFTVSTWEGQKSKTLESLMQYSEPRIHFTPEKFPQNNPRSLVKRTIQLKRTHTATG 230
QY 237 INVVAIVEFBEELGAPDARKVLIIITDGR--ATDSGNIDAAD----IIRYIIGIGKA 289
DB 231 IRRVVELFNTTNGARKNAFKIIVITDGEKFGDPLGEYEVIREADREGYIRVYIGVDA 290
QY 290 FOTKESQETLHKFASPKASEFVKIILDTFEKLKDLFTELQKIIVYIGSTSKQDLSPFMBL 349
DB 291 FREKSRQELNLTASKRPPDHVFPQNNFEALKTIONQREKIFALIBSTQSSSFEHEM 350
QY 350 SSGISADLSRGAHVAVGAGKDMAGFLDLKADLDODPTEIGNEPLTEVRAGVLYTVT 409
DB 351 SGEFSALITNSGPBLSTVGSYDMAGVF-LYTSKEXSTFINMTRVDSMDNDAYLGFAAA 409
QY 410 WLPDRQKTSILASGAPRYQMGKRVLLFOEPQGGHMSQVOTINGTOIGSYFGSELGVNV 469
DB 410 -ILRRRVOSLVVGAPRYQHIGVAMFR--QNTGMESNANVXGTOIGAFYGASLSCVDV 466
QY 470 DQGETELLIGAPLFGYBGRGRVFIY-----ORQLGFEYSBLQDGGYVLGRGEA 524
DB 467 DSNGSTDLVIGAPHYEBQTRGQVSCPLPRQGRAMWQCDAY--LYGEGQGWGRRGAA 524
QY 525 ITALTINGDGLVAVVGAFLER--OGAVYIFNGRHG-GHSPOBQRIBSTQVLSGIOWF 581
DB 525 LTVLGDVNGDKLDVAIGARBEDNKGAVLPHGTSGSGISPSHSQRIAGSKSLPRLOVF 584
QY 582 GRSIHGVKDLGDLADVAVGASQMTVLSRPVDMVTLMFSFPAEIPVHEVCYSTS 641
DB 585 GQELSGGQDLTMQGLVDLTVGAQGHVLLRSQVLRKALIMFRPREVANVECDQV 644
QY 642 NQKKEGNITICPOI--KSLVPOF--QGLVLANLYTTLQDGHRTRRRLPFGGHELRNI 659
DB 645 -KQKEGEVAVVCLAVQKSTRDLREBQIQSVVYTDLALDSGRHSRAVEFETKNSSTRQT 703
QY 700 AVT-TSMSCDTFSFHPVVCVODLISPIVNSLSLMEBETPRDQACQKDIPIILPSL 758
DB 704 QVTLGTLQCTLKLQLPNCIEDVPSPIVLANFSL---VETPLS--AFGN-----LRPV 753

```

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QY 759 HSETWEI-----PEKNCGEKCKEANTLRVSPSPARBARLRTAFASLSVELSLNLEED 813
DB 754 AEDAQRLFLALFPFKKCGNDNICDDLTSTTFMSLDCLVGGRPEFNVTVVRDGED 813
QY 814 AYVWQDLHFPPLSPKXVEML---KPSQIPVSCBELPEESRLLRAL---SCNVSSPI 867
DB 814 SYRTQVTFPPLDLSRYKSTLQNGRSQSRWLACSS--ASSYEVGALKSTSCSINHPI 871
QY 868 FKAGHSVALQMMNTLVNSWGDSEVLHANTVCNEDSDILENSATTT--IPILYPIN 924
DB 872 FPNSEVTFNITPDVSKASISGKLLKXNVISENN---MPTNTTEFQLELPVKAAY 927
QY 925 ILIQDQEDSTLYVFTPKPKKINQKMGVQVRLQPSIHNDIPTLEAVVGVPQPSRGP 984
DB 928 MVTSHGVSTKYLNFTASERTSRWQHGYOV---SNIGQSLP-ISLVFLVPLVNLQTVI 983
QY 985 THQMSVQMBEPV--PCHYEDLERLPDAEPCPLPGALFRCPV----- 1024
DB 984 WDRPQVTFPSNLSSTGHTK--ERLPESHQ--FLAEIRKAPVNVCSIAVQCRIGCDIPFG 1039
QY 1025 FROELIVQYIGLELVGEIEBAS-SMFSLGSLSISFNSSKHFLYGSNLSL-AQVVKVD 1082
DB 1040 IQREFNATLKGNLSFPMYIKTSHNHLLIVSTAILELFDNSVFTLLPGQAFVRSQTEKYE 1099
QY 1083 VVYEKQMLVLYVSGIGLILLLIFIVLYKGFPRKNIKKEKAEGRGVNGIP 1136
DB 1100 PFEVNPPLLVGSSVGGILLALITPALLYKLGFFRQYKDMWSEG-GPGABP 1152

```

RESULT 13  
 US-08-482-293A-3  
 Sequence 3, Application US/08482293A  
 Patent No. 5831029  
 GENERAL INFORMATION:  
 APPLICANT: Gallatin, W. Michael  
 APPLICANT: Van der Vieren, Monica  
 TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
 NUMBER OF SEQUENCES: 103  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 233 South Wacker Drive, 6300 Sear Tower  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/482,293A  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/173,497  
 FILING DATE: 23-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/286,889  
 FILING DATE: 5-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/362,652  
 FILING DATE: 21-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Williams Jr., Joseph A.  
 REGISTRATION NUMBER: 38,659  
 REFERENCE/DOCKET NUMBER: 27866/32684  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 1153 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-482-293A-3

Query Match 25.6%; Score 1563; DB 2; Length 1153;  
 Best Local Similarity 34.3%; Pred. No. 1,9e-124;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

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QY 6 ITTAMALLSGFFFPAPASSYNDIVGARSFSPPRAGHGVLYQV-GNGVIVAGGE- 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   6 ILLTALTLCHGF-----NLDTEAMTFQ--ENNRGFGSVVQLQGRVVVGAQOEI 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 --GNSGSLVQCCSGHCHLPTLR-GSNTSKYLGTTLATDTPDGSILACDGLSRTCD 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   55 VAANRGSLVQCCVYSTSCSPRIQLQVVEAVNMSLGLSLATTSPPQLACGFTVHTCS 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFQECIKG---NVDLVFLFDGMSLQDPDEPKIL 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   115 ENTYYVGLGCLFPSNLR-----QQPKQEPFALRGCPQEDSDIATLIDSSGSIIDHPRRMK 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 DEPKDVKKLSNTSYQPAVQSTSYKTEFSDYVKRKPDAALKHVKMLLTNTFGA 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   171 EFVSTVMEQLKSKRTLFSLMQLYSEEFRIHFTFKEPQNNPRLVKPITQLLGRTHATG 230
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 237 INVVAEVPFEELGARDATKVLIIITDGE--ATDSGNIDAAND---IIRYIIGIKH 289
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   231 IRVVELEFITTGARKNAKILVITDGEKPGDPLGEVIRPADREGVIRVIGVDA 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 290 FQTKESQETLHAKSPASEFVKILDTFEKLDLFTLQKKIYVIGSTSKQDLPFMEL 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   291 FPEKSKQELANTLASKPRPHVFOVNNFEALKTIQNLARKETALIBSTQSSSFEHEM 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 350 SSSGISADLSRGNAVVGAKQWAGGFLLDKADLQDDFTIGNEPLTPVRAGYLTVT 409
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   351 SGRGFSALITNSGPLSLSTVGSYMWAGVF--LYTSKSKSTFINMTRVSDMNDAYLVGAAA 409
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 410 WLPSSRQKTSLLASGAPRYOMGRVLLFQEPQGGHMSQVQITIGTOISGFSEGLGVNDV 469
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   410 -ILLRNKVGSLVAGAPRYQHIGLVAMFR--QNTGMESNANVNGTQIGAFGASLGSVDV 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 470 DQDQETELLIGAPLFYGEORGRVFYI-----QRQLGFEVSELOQDGPYLGFRGEA 524
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   467 DSKGSDTLVLIGAPHYEQTRGQVSCPLPRGQRARWQCDAY--LYGEGQGWGRGA 524
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 525 ITALTIDINGDLVDVAVGAPLEE--QGVYITFNGRHG-GLSPQSORICTQVLSGIQWF 581
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   525 IATVIGVNGDKLTDVAIGAPGEEENRGAVYLFHGTSGSGISPSHSQRLASGLSPRLQYF 584
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 582 GRSHVQKDLGEGGLADVAVGAESOMTVLSRPVDMVTLMSSPAEIPVHEVCASSTS 641
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   585 GQSLSGQDILTMGLVDLVGAQGHVLLLSQPLRKALMERNPREVANVEKCDQV 644
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 642 NKKMEGVNITICFOI-KSLYPOF-QGRLVANLTYTTLQDGHTRRRGLFGCHHELARNI 699
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   645 -KQKEAGVAVCLHVQKSTDRDLREGLQISVVYTDLALDGRPHSRVAFETNSTRQF 703
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 700 AVT-TSMSCDTSFHFHPVCVQDLISPIVNSLSLWEEESTPRDQAGKDIPIILPSTL 758
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   704 QVGLQTCETKLQQLPNCIEDPVSPIVLRNLSL--VQTPLS--AFGN-----LRPVL 753
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 759 HSETWEL-----PEKKGCGDKXCEANLRSFSPARARALRLAFASLSYELSLNLEED 813
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   754 AEDAQRFLTALFPPEKKGCDNMCQDLSITFSMSLDCVVGQPREFNTVTVVRDGED 813
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 814 AYWVQDLHPPGLSPFKVEML--KPHSQIPVSCBELPRESRLSRAL--SCNVSSPI 867
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   814 SYRTQVYFFFPDLSTKRVSTLQNGRSQRWRLACES--ASSTEVSAALSTGCSINHPI 871
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 868 FKAGHSVALQMMFNTLVNWSGDSVBLHANVTCCNEDSDILLENSATTT--IPILYPIN 924
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

DB 872 PRENSEVENTETFDVDSKASLGKLLKANVTSENN---MBRTNTEFOLELPVKYAVY 927
QY 925 ILLQDQEDSTLYVSPFKPKXIHQVKNVQVRIQPSIHDNIPTLEAVVGVPQPESECP 984
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   928 MYVTSHGVTKYINFPASENTSRWMOHQYV--SNLQGRSLP-ISLVLVVPRLANQYVI 983
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 985 THQMSVQMBPVV--PCHYDELERLPDAAPCULGALFRCPVV----- 1024
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 984 WRPQVTFPENSISTCHTK--ERLPSHD--FLAELRKAPVNVNCSIAVCRIQCDIPFG 1039
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1025 FROELIVQYITGLVGLGEIEAS-SMPSLCSLSISPSKHLVGSNLSL-AQVVMKTD 1082
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1040 IOEBFNAATLKGMSLSPDMYIKTSHNMLIVTAEIILFNDSVFTLLPQGAFAVSQETTKYE 1099
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1083 VYEEKOMLYLVYLSGIGLLLLLFYLVYKVGFPKRNKEMKAGRGVNPNGIP 1136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1100 PREVPNPFLVIGSSVGLLLALLITALYKLGFFKRYKDMMSBG-GRPGARP 1152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 14
US-08-943-363-3
; Sequence 3, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-3
Query Match 25.6%; Score 1563; DB 2; Length 1153;
Best Local Similarity 34.3%; Pred. No. 1,9e-124;
Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

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QY 6 ITWAMALLSGFFFPADASSYNLDVRGARSFSPRAGRHRGYVLQV-GNGVIVGABGE- 63
DB 6 LILFALTALCHGF-----NIDTENAMTFQ--ENARGGQSVVQLQSGRRVVGABGEI 54
QY 64 --GNGSTSLVQCGSGTGHCLPVTLR--GSNYTSKYLGNTLATDPTDGSILACDPLGSRCTD 120
DB 55 VAANQSGSLVQCGVSTGSCPIRLQVPEAVNMSLGSLAATTSPPQLACGPTVHQTCS 114
QY 121 QNTYLSGLCTLPFQNLQGPMLQGRPGFQECIKG---NVDLVLFPDGSMSLQDPEQKIL 176
DB 115 ENTYYKGLCFPLFGSNLR-----QOPQKPEALRGCPQEDSDIAFLIDSGSIIIPHDFRMK 170
QY 177 DFMKWDKLSNYSYQPAVQFSTYKTEPDPFSDYVRKDPDALLKVKHMLLTJNFGA 236
DB 171 EFVSTVMEQLKSKTLPMLQYSEEFRIHFTFKSFQNNPNRSLVKCITDGLGTHRTATG 230
QY 237 INVYATEVPREBELGARPDPATKVLIIITDGE--ATDSGNIDAAD-----IIRYIIGIKH 289
DB 231 IRKVRRELFINITNGARKNAFKILVITDGEKFGDPLGEVDIPEADREGVIRYIVGDA 290
QY 290 FQTKESQETLHKAASKPASEFVKILDTPEKLDLFTLEOKKIYIEGTSKODLTSFMEL 349
DB 291 FRSEKSHQELNTIASKEPRDHVFQVNNFELKTIQNLREKIPAIEGTQSSSSSFHEM 350
QY 350 SSSGISADLSRGHNVGAVGAKMAGFBLDKADLDDPTFIGNRPLPEVRAGLYGTYT 409
DB 351 SQEGFSALITSNGBLSTVGSYDMAGVF--LYTSKESKSTFIMNTRVSDMNDALGFAA 409
QY 410 WLPSPKSTSLASGAPRYOHMGVRLFOEPQGGHMSOVQTIHGTOIGSYFGEELGVDV 469
DB 410 -IILRRVQSLVVGAPRYOHIGLVAMFR--QNTGMESNANVGTQIGAFGASLCSVDV 466
QY 470 DQDGETELLIGAPLFYGEORGRVFY-----QRQLGFEVSELOQDPGYLGRGEA 524
DB 467 DSNGSTDLVILIGAPHYEGOTRGQVSVCP--PRGGRAMQCDV--LVGEGQGPWGRGAA 524
QY 525 ITALTDINGGLVDVANGAPLEE--QNAVITENGRRH--GLSPQSQRIEGTQVLSGIQMF 581
DB 525 LTYLGVNKGKLDVAGAPGEBEDNRGAVYLFHGTSGSGISPSISQIASKSPRLQYF 584
QY 582 GRSIHGVKDEGDLAVVAGASQOMVLSSRPVVDVTLMSFSPARIPEHVECSYSTS 641
DB 585 GQSLSGQDLDMDGLVDLVGAGQHVLLRSQPLAKALMEFVREAVARVEECNOVV 644
QY 642 NKKEGVNITICFOI--KSLYPOF--QGRVANTLYTTLQDGRTRRRGLFGGRHELEARNI 699
DB 645 --KKGKAGEVAVCLHVQSTRDLREBQIGQSVYTYDLALDSGRPHSRVAFMETKSTRQT 703
QY 700 AVT--TMSCTDFSGHFVVCVODLISPLNVSINFSLMEEBGTPRDQAGKDIPIILPSL 758
DB 704 QVGLTQTCETLKLQLPNCIEDPVSPVLRLNFSL--VGTPLS--AFGN-----LAPVL 753
QY 759 HSETEWEL-----PREKKGEGDKCEANLAVSFPARSARALRLTAPASLVELSLNLEED 813
DB 754 AEBDAQRLFTLAPPEKNGCNDNITCQDDLSTFSPMSIDCLVAGGPREFNVTYVRNGED 813
QY 814 AYWVQDLHFPFGISFEXKVEL--KPHSOI--PVSCEELPEBSRLISRAL--SCNVSP 867
DB 814 SYTQVTFPFLDLSYKVGSTLQNGRQSRMLACES--ASSTVSGALSTGSSINHPI 871
QY 868 FKAHSHVALQMFNTLVNSSMGDSVELHANTVCNEDSDLLIEDNSATTT--IPILYPIN 924
DB 872 FPENSEVTFNITPEVDSKASIGNKLILKANTVSENN--MPRTNKTPEOLELPEVKAAYV 927
QY 925 ILIQDQDSTLYVSEFPGKPIHQVKMYOVRLOPSIHDNIPFLAEVAVGPPSPSGPI 984
DB 928 MVTVSHGVSTKILNLTASNTSRVMOHQOV--SNLQGRSLP--ISLVFLVPRALNQTVI 983
QY 985 THQMSVQMEBPV--PCHYEDLERLDAAPCLPGLFRCPV-----1024
DB 984 MDRQVTFPSENLSTGHTK--ERLPSHD--FLAEKAPAVNVSINAVQRIQCDIPFG 1039

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QY 1025 PROEILVQVIGTLELVEIAS--SMFSLCSSLISFNSGHPHYGSNALL--AQVWVKD 1082
DB 1040 IOEFNATLKNLSFDMYIKTSHNHLIVSTAILPRDSIPTILLPGGAVRQOTERVE 1099
QY 1083 VYREKOMLYLVYLSIGIGLLLLLIPIVLVYKVGFFKRNLEKKEAGRGVENGIP 1136
DB 1100 PFEVNPPLPVLVGVSSVQGLLLALLITALYKLGFFPKQYKQYDMMSSEG--GPGABP 1152

RESULT 15
US-09-193-043-3
; Sequence 3, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vliet, Monica
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193, 043
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-193-043-3

Query Match      25.6%; Score 1563; DB 3; Length 1153;
Best Local Similarity 34.3%; Pred. No. 1.9e-124;
Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

QY 6 ITWAMALLSGFFFPADASSYNLDVRGARSFSPRAGRHRGYVLQV-GNGVIVGABGE- 63
DB 6 LILFALTALCHGF-----NIDTENAMTFQ--ENARGGQSVVQLQSGRRVVGABGEI 54
QY 64 --GNGSTSLVQCGSGTGHCLPVTLR--GSNYTSKYLGNTLATDPTDGSILACDPLGSRCTD 120
DB 55 VAANQSGSLVQCGVSTGSCPIRLQVPEAVNMSLGSLAATTSPPQLACGPTVHQTCS 114
QY 121 QNTYLSGLCTLPFQNLQGPMLQGRPGFQECIKG---NVDLVLFPDGSMSLQDPEQKIL 176
DB 115 ENTYYKGLCFPLFGSNLR-----QOPQKPEALRGCPQEDSDIAFLIDSGSIIIPHDFRMK 170
QY 177 DFMKWDKLSNYSYQPAVQFSTYKTEPDPFSDYVRKDPDALLKVKHMLLTJNFGA 236
DB 171 EFVSTVMEQLKSKTLPMLQYSEEFRIHFTFKSFQNNPNRSLVKCITDGLGTHRTATG 230
QY 237 INVYATEVPREBELGARPDPATKVLIIITDGE--ATDSGNIDAAD-----IIRYIIGIKH 289
DB 231 IRKVRRELFINITNGARKNAFKILVITDGEKFGDPLGEVDIPEADREGVIRYIVGDA 290
QY 290 FQTKESQETLHKAASKPASEFVKILDTPEKLDLFTLEOKKIYIEGTSKODLTSFMEL 349
DB 291 FRSEKSHQELNTIASKEPRDHVFQVNNFELKTIQNLREKIPAIEGTQSSSSSFHEM 350
QY 350 SSSGISADLSRGHNVGAVGAKMAGFBLDKADLDDPTFIGNRPLPEVRAGLYGTYT 409
DB 351 SQEGFSALITSNGBLSTVGSYDMAGVF--LYTSKESKSTFIMNTRVSDMNDALGFAA 409
QY 410 WLPSPKSTSLASGAPRYOHMGVRLFOEPQGGHMSOVQTIHGTOIGSYFGEELGVDV 469
DB 410 -IILRRVQSLVVGAPRYOHIGLVAMFR--QNTGMESNANVGTQIGAFGASLCSVDV 466
QY 470 DQDGETELLIGAPLFYGEORGRVFY-----QRQLGFEVSELOQDPGYLGRGEA 524

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[illegible]

Search completed! August 30, 2005, 11:53:02  
Job time : 51 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: August 29, 2005, 19:15:58 ; Search time 29 Seconds

(without alignments)  
3881.849 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106

Sequence: 1 MKDSCITVMANALSGFFRF.....DPGLKPLHEDSGSGGKD 1170

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : PIR 79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	6098	99.9	1170	2	cell surface glyco
2	4343.5	71.1	1163	2	lymphocyte function
3	1563	25.6	1153	1	cell surface glyco
4	1526.5	25.0	1163	1	cell surface glyco
5	1514.5	24.8	1153	2	leukocyte surface
6	1114.5	18.3	1151	2	integrin alpha-1 c
7	1112.5	18.2	1180	2	integrin alpha-1 c
8	1012.5	16.6	1170	2	integrin alpha-2 s
9	985	16.1	1181	2	integrin alpha-2 c
10	976.5	16.0	1179	2	integrin alpha-2 c
11	959	15.7	1178	2	integrin alpha-2 c
12	678.5	11.1	1035	2	integrin alpha-9 c
13	633	10.4	1039	2	lymphocyte-Peyer's
14	619.5	10.1	1038	2	integrin alpha-4 c
15	588	9.6	1041	2	integrin alpha-4 c
16	557.5	9.1	1041	2	integrin alpha-4 c
17	546	8.9	1137	2	alpha-7 integrin -
18	536.5	8.8	1051	2	integrin alpha-7 c
19	536.5	8.8	1051	2	cell surface glyco
20	530	8.7	1049	2	integrin alpha-3 c
21	522	8.5	1053	2	fibronectin recept
22	521.5	8.5	1054	2	WLA-3 alpha subun
23	508.5	8.3	1106	2	integrin alpha-5 c
24	487	8.0	1053	2	integrin alpha-5 c
25	480.5	7.9	1037	2	glycoprotein IIB -
26	478	7.8	1039	2	integrin alpha-2b
27	476.5	7.8	1394	2	position-specific
28	473.5	7.8	1146	2	integrin - fruit f
29	467.5	7.7	1044	2	integrin alpha-8 c

30	463.5	7.6	1073	2	integrin alpha-6 c
31	462.5	7.6	1072	2	integrin alpha-6 c
32	460	7.5	1034	2	integrin alpha-V c
33	451.5	7.4	1226	2	F54F2.1 protein -
34	449.5	7.4	1091	2	integrin alpha-6 c
35	437.5	7.2	1115	2	integrin alpha-6 c
36	436.5	7.1	1044	2	integrin alpha-v c
37	434.5	7.1	1045	2	integrin alpha-v c
38	433.5	7.1	1115	2	integrin alpha v c
39	419	6.9	764	2	integrin alpha cha
40	408	6.7	1048	2	glycoprotein IIB -
41	384.5	6.3	1139	2	integrin alpha-5 c
42	343	5.6	1086	2	hypothetical prote
43	296.5	4.9	604	2	integrin alpha cha
44	251.5	4.1	272	2	glycoprotein IIB -
45	244	4.0	3124	2	integrin alpha-1 -
					collagen alpha 1(X

## ALIGNMENTS

RESULT 1  
S03308  
cell surface glycoprotein CD11a precursor - human  
M:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text\_change 09-Jul-2004  
C:Accession: S03308; A47458; A47565; A48759; S36044  
R:Larsen, R.S.; Corbi, A.L.; Berman, L.; Springer, T.  
J Cell Biol. 108, 703-712, 1999  
A>Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit  
A:Reference number: S03308; MUID:89139587; PMID:2537322  
A:Accession: S03308  
A:Molecule type: mRNA  
A:Residues: 1-1170 <L&R>  
A:Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:G31421; P1DN:CAA687-  
A:Note: part of this sequence was confirmed by protein sequencing  
R:Corriveau, R.D.; Gollub, K.A.; Hickey, D.D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993  
A>Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pro-  
A:Reference number: A47458; MUID:92248261; PMID:8097887  
A:Accession: A47458  
A:Molecule type: DNA  
A:Residues: 1-20 <COR>  
A:Note: sequence extracted from NCBI backbone (NCBI:130862, NCBI:130863)  
R:Shelley, C.S.; Farokhzad, O.C.; Arnout, M.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993  
A>Title: Identification of cell-specific and developmentally regulated nuclear factors ti-  
A:Reference number: A47565; MUID:93281759; PMID:8099450  
A:Accession: A47565  
A:Molecule type: DNA  
A:Residues: 1-20 <SHS>  
A:Cross-references: GB:M95609  
R:Noda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.  
J. Biol. Chem. 268, 19305-19311, 1993  
A>Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.  
A:Reference number: A48759; MUID:93374910; PMID:8103515  
A:Accession: A48759  
A:Molecule type: DNA  
A:Residues: 1-20 <NUE>  
A:Cross-references: EMBL:Z22804; NID:G311405; P1DN:CAA80461.1; P1D:G311406  
C:Genetics:  
A:Gene: GDB:ITGAL; CD11A  
A:Cross-references: GDB:119757; OMIM:153370  
A:Map position: 16p11.2-16p11.2  
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo  
C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tra  
F1-25/Domain: signal sequence #status predicted <Sig>  
F126-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted <?>  
F1154-317/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 99.9%; Score 6098; DB 2; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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Qy	61	PGEKNGSTSLVQCQSGTGCHLPVTLRGSNTSKYLGMTLATPDTPGSLIACDPGLSRTCD	120
Db	61	PGEKNGSTSLVQCQSGTGCHLPVTLRGSNTSKYLGMTLATPDTPGSLIACDPGLSRTCD	120
Qy	121	QNTLISGLCTYPRQNLQCPMLQGRPGFQECIKANDVLVLPFDGSMGLPDPFQKLTDPMK	180
Db	121	QNTLISGLCTYPRQNLQCPMLQGRPGFQECIKANDVLVLPFDGSMGLPDPFQKLTDPMK	180
Qy	181	DVMKGLSNTSYQFAVQSTSKYTFEFDSDYKRDPAALLKHVGMMLLNTTGAIVYV	240
Db	181	DVMKGLSNTSYQFAVQSTSKYTFEFDSDYKRDPAALLKHVGMMLLNTTGAIVYV	240
Qy	241	ATEVPRRELGARPDATKVLIIITDGEANDSGNIDAAKDIIRYIIGIGHFQTKESQETLH	300
Db	241	ATEVPRRELGARPDATKVLIIITDGEANDSGNIDAAKDIIRYIIGIGHFQTKESQETLH	300
Qy	301	KPASKPASEFYKILDTFEKLKDLFTELQKTYVIEGTSKODLTSFNMELSSSGISADLSR	360
Db	301	KPASKPASEFYKILDTFEKLKDLFTELQKTYVIEGTSKODLTSFNMELSSSGISADLSR	360
Qy	361	GHAUVGAAGAKOMAGFLDLKADLDDDTFIGNELTPPEVRAGYLGATYTWLPSROKTSLL	420
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Qy	421	ASGAPRYOMGRVLLFOEPQGGHMSQYQTIHGTOIGSYFGGELCGVVDODGEETLLI	480
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Qy	481	GAPLFYQGRGGRVFIYQRRQLGFEEVSELQDPEYPIGRGEBATLTALTINGDGLVVA	540
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Qy	541	VGAPLEEGGAYYIFNGRHGSLSPQPSQRIEGTOVLSGIQWFGRSIHGVKDLBGDGLAVVA	600
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Qy	601	VGASQOMTVLSRPVVDVTLMSFSPARI PVHEVCSYSTSNKMGVNTICFOIKSLY	660
Db	601	VGASQOMTVLSRPVVDVTLMSFSPARI PVHEVCSYSTSNKMGVNTICFOIKSLY	660
Qy	661	POFQGRVLAANTYTLQDLGHRTRRGLPFGGRHELRNI AVTSSMCTDPSFHFVVCVD	720
Db	661	POFQGRVLAANTYTLQDLGHRTRRGLPFGGRHELRNI AVTSSMCTDPSFHFVVCVD	720
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Qy	781	LRVSPSPASRALRLTAFASSVSELSTNLBEDATWVOLDLHFPPLGFRKVKMLKPHSQ	840
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Db	901	NNEDSDLEDNSATTIIPILYPINLIDQDEBSTLYVFTPKGPKIHQVKHMYQVRIOPS	960
Qy	961	IHDHNIPTLEAVVGPQPSSEGPITHQMSVQMEPPVPCHEYEDLELPPAAEFCLPGALFR	1020
Db	961	IHDHNIPTLEAVVGPQPSSEGPITHQMSVQMEPPVPCHEYEDLELPPAAEFCLPGALFR	1020
Qy	1021	CPVVFROEILVQVIGTLEVGEIEASSMFSLCSSLSISFNSKHFHLVGSNASLAQVVMK	1080
Db	1021	CPVVFROEILVQVIGTLEVGEIEASSMFSLCSSLSISFNSKHFHLVGSNASLAQVVMK	1080

Qy	1081	VDVYERQMTLYLVLSIGIGLLLLLIIFIVLYKVFERNLKEKMEAGRGVNGIPAEBS	1140
Db	1081	VDVYERQMTLYLVLSIGIGLLLLLIIFIVLYKVFERNLKEKMEAGRGVNGIPAEBS	1140
Qy	1141	EQLASQGEADPGCLKPLHEKDESGGGKD	1170
Db	1141	EQLASQGEADPGCLKPLHEKDESGGGKD	1170
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156126			
Lymphocyte function-associated molecule-1-alpha - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004			
C:Accession: 156126			
R:Kaufman, Y.; Tseng, E.; Springer, T.A.			
J: Immunol. 147, 369-374, 1991			
A:Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit ar			
A:Reference number: 156126; MUID:91268576; PMID:2051027			
A:Accession: 156126			
A:Status: preliminary; translated from GB/EMBL/DBJ			
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A:Cross-references: UNIPROT:P24063; GB:M60778; NID:G198785; PIDN:AAA39426.1; PID:G198786			
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Best Local Similarity 72.8%; Pred. No. 7,7e-292;			
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Db	11	LLLSGLQFAVAMSYNLDTRPTQSEFL-AQAGRHFQYQVLTIEDGVVGAPEGNDTGGILYH	69
Qy	73	COSGTGCHLPVTLRGSNTSKYLGMTLATPDTPGSLIACDPGLSRTCDQNTYLSGLCYLF	132
Db	70	CRISSECPQVPSLSHSGNHTSKYLGMTLATDAKSLACDPGLSRTCDQNTYLSGLCYLF	129
Qy	133	RQNLQGMLOGRPFQECIKANDVLVLPFDGSMGLQDPEFOKLTDPFKMDVWKKLSNTSYQ	192
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Qy	193	FAAVQSTSKYTFEFDSDYKRDPAALLKHVGMMLLNTTGAIVYVATEVPRRELGA	251
Db	190	FAAVQSTSKYTFEFDSDYKRDPAALLKHVGMMLLNTTGAIVYVATEVPRRELGA	249
Qy	252	RPDXTKVLIIITDGEANDSGNIDAAKDIIRYIIGIGHFQTKESQETLHFKPASKPASEFV	311
Db	250	RPDXTKVLIIITDGEANDSGNIDAAKDIIRYIIGIGHFQTKESQETLHFKPASKPASEFV	309
Qy	312	KILDTFEKLKDLFTELQKTYVIEGTSKODLTSFNMELSSSGISADLSRGAHVAVGAYGAK	371
Db	310	KILDTFEKLKDLFTELQKTYVIEGTSKODLTSFNMELSSSGISADLSRGAHVAVGAYGAK	369
Qy	372	DWAGGFLDLKADLDDDTFIGNELTPPEVRAGYLGATYTWLPSROKTSLLASGAPRYOMG	431
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Qy	432	RVLVLFQRPQGGHMSQYQTIHGTOIGSYFGGELCGVVDODGEETLLIIGAPLYGSGORG	491
Db	430	RVLVLFQRPQGGHMSQYQTIHGTOIGSYFGGELCGVVDODGEETLLIIGAPLYGSGORG	489
Qy	492	GRVFIYQRRQLGFEEVSELQDPEYPIGRGEBATLTALTINGDGLVVAAGAFLPEEGAV	551
Db	490	GRVFIYQRRQLGFEEVSELQDPEYPIGRGEBATLTALTINGDGLVVAAGAFLPEEGAV	549
Qy	552	YIFNGRHGSLSPQPSQRIEGTOVLSGIQWFGRSIHGVKDLBGDGLAVAGASQMTVLS	611
Db	550	YIFNGRHGSLSPQPSQRIEGTOVLSGIQWFGRSIHGVKDLBGDGLAVAGASQMTVLS	609



QY 612 SRPVDMNTLMSPFPAETPVHEVECSYSTSNMKEGVNITICFOIKSLYPOQGRVNL 671  
 DB 610 SRPVDMNTLMSPFPAETPVHEVECSYSTSNMKEGVNITICFOIKSLYPOQGRVNL 669  
 QY 672 TTTTLDGHRTRRGLFPGGRHLEARNIAVTTSMCTPFSFFPVCVODLSPINVSINF 731  
 DB 670 SYTLDDHGRMRKRLFPDGSHELSGNISITPDKCLDPHFHFPICIDILSPINVSINF 729  
 QY 732 SLMEEGTPRDQRAQKDIPIILRSLHSETWEIPEKXNGCEKXCEANLRVFSFASR 791  
 DB 730 SLMEEGTPRDQRAQKDIPIILRSLHSETWEIPEKXNGCEKXCEANLRVFSFASR 786  
 QY 792 ALRLTAPASLSVELSLNLEBAYVVDLHPPLGSLRKYMKLKPQSLPVSCGELEEB 851  
 DB 797 PLRLMSASLAVEMWLTNSGEDAYVWRDLDPRLGSLFRKYMKLQPHSRMPVSCGELEEG 846  
 QY 852 SLRLSALSCNVSPIFRAGHGVVALQMMFNTLVNSMGDSVELHANYTCNNEDSDLEDN 911  
 DB 847 SLRLSALSCNVSPIFRAGHGVVALQMMFNTLVNSMGDSVELHANYTCNNEDSDLEDN 906  
 QY 912 SATTIIPILYPIINILIDQEDSTLYVSTPKGPKLHYVMYQVRIOPSIDHNIPITLEA 971  
 DB 907 SAATHIPVLYPVNLTKEGENTLTVISFPKPKQVQVHYQVRIOPSAYDHNPITLEA 966  
 QY 972 VVGVPQPSSEPTIQMSVQMEPPVPCYEDLER-LPDAEPCLFGLFRCVVRQRIIL 1030  
 DB 967 LVGVPRPSEDLITVWSVQTDPLVLTCHSEDLKRPSSSEAPCLPQVGFRCPIVRWEIL 1026  
 QY 1031 VOYIGTLENGEIEKSMPSICSSISIPNSKHLVGSNLAOVYMKVYVEKML 1090  
 DB 1027 IGVNITVELSKETKASTSTLSSISVSPNSKHLVGSNLAOVYMKVYVEKML 1086  
 QY 1091 YLYVLSGIGLILLLIFIVLYKVGFPRKMLEKMEKAGVNGIPAEDEOLA-SGOEA 1149  
 DB 1087 HVTYVLSGIGLILLLIFIVLYKVGFPRKMLEKMEKAGVNGIPAEDEOLA-SGOEA 1146  
 QY 1150 GDPEGLKLP 1157  
 DB 1147 KDMGCLER 1154  
 RESULT 3  
 RNU1B  
 cell surface glycoprotein CD11b precursor [validated] - human  
 N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac  
 eukocyte integrin alpha chain; neutrophil adherence receptor alpha chain  
 C:Species: Homo sapiens (man)  
 C:Dates: 31-Dec-1992 #sequence, revision 31-Dec-1992 #text change 09-Jul-2004  
 C:Accession: A31108; A28915; A41600; A20892; A32218; A46526; A26091; 152567  
 R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.  
 J. Biol. Chem. 263, 12403-12411, 1988  
 A>Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD  
 B.  
 A:Reference number: A31108; MUID:88315033; PMID:2457584  
 A:Accession: A31108  
 A:Molecule type: mRNA  
 A:Residues: 1-1153 <COR>  
 A:Cross-references: UNIPROT:P12125; GB:J03925; NID:9187284; PIDD:AAA59544.1; PID:9307148  
 A>Note: part of this sequence was confirmed by protein sequencing  
 R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.  
 J. Cell Biol. 106, 2153-2158, 1988  
 A>Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor M  
 A:Reference number: A28915; MUID:88257215; PMID:2454931  
 A:Accession: A28915  
 A:Molecule type: mRNA  
 A:Residues: 1-499,501-965, 'P', 967-1153 <ARN>  
 A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:9186935; PIDD:AAA594  
 A>Note: the authors translated the codon TAC for residue 1129 as Thr  
 R:Shelley, C.S.; Arnaout, M.A.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 10525-10529, 1988  
 A>Title: The promoter of the CD11b gene directs myeloid-specific and developmentally reg

A:Reference number: A41600; MUID:92073318; PMID:1663702  
 A:Accession: A41600  
 A:Molecule type: DNA  
 A:Residues: 1-9 <GHE>  
 A:Cross-references: GB:M76724; NID:9180018; PIDD:AAA58410.1; PID:9553215  
 R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988  
 A>Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesion  
 A:Reference number: A94193; MUID:88190151; PMID:2833753  
 A:Accession: A30892  
 A:Molecule type: mRNA  
 A:Residues: 917-1042 <AR2>  
 A:Cross-references: GB:M18044  
 R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989  
 A>Title: cDNA sequence for the alpha subunit of the human neutrophil adherence receptor  
 A:Reference number: A32218; MUID:89098893; PMID:2563162  
 A:Accession: A32218  
 A:Molecule type: mRNA  
 A:Residues: 9-1153 <HIC>  
 A:Cross-references: GB:U04145; NID:9189068; PIDD:AAA59903.1; PID:9386975  
 A>Note: part of this sequence was confirmed by protein sequencing  
 R:Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.  
 J. Immunol. 150, 480-490, 1993  
 A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in  
 n during evolution.  
 A:Reference number: A46526; MUID:93123748; PMID:8419480  
 A:Accession: A46526  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-499,501-1153 <FLB>  
 A:Cross-references: GB:S52227; NID:9263047; PIDD:AA24821.1; PID:9263049  
 A>Note: the last three bases of intron 13, CAG, are included in some but not all mature  
 A>Note: sequence extracted from NCBI backbone (NCBI:P:121963)  
 R:Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.  
 Biochim. Biophys. Acta 874, 368-371, 1986  
 A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp  
 A:Reference number: A90664; MUID:87076671; PMID:3539202  
 A:Accession: A26091  
 A:Molecule type: protein  
 A:Residues: 17-31 <PIE>  
 A:Experimental source: granulocytes  
 R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.  
 Blood 79, 865-870, 1992  
 A>Title: Characterization of the myeloid-specific CD11b promoter.  
 A:Reference number: 152567; MUID:92144986; PMID:1346576  
 A:Accession: 152567  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-9 <RES>  
 A:Cross-references: GB:M04477; NID:9180184; PIDD:AAA51960.1; PID:9553219  
 C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1  
 C:Genetics:  
 A:Gene: GDB:ITGAM; CR3A  
 A:Cross-references: GDB:120599; OMIM:120980  
 A:Map position: 16p11.2-16p11.2  
 A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites  
 C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo  
 C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag  
 P:11-16/Domains: signal sequence #status predicted <SIG>  
 P:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>  
 P:117-1108/Domains: extracellular #status predicted <EXT>  
 P:148-318/Domains: von Willebrand factor type A repeat homology <VWA2>  
 P:465-473/Region: calcium/magnesium binding #status predicted  
 P:530-538/Region: calcium/magnesium binding #status predicted  
 P:593-601/Region: calcium/magnesium binding #status predicted  
 P:1109-1134/Domains: transmembrane #status predicted <TM>  
 P:1115-1153/Domains: intracellular #status predicted <INT>  
 F:86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding  
 Query March 25.6%; Score 1563; DB 1; Length 1153;  
 Best local similarity 34.3%; Pred. No. 1,9e-99;  
 Matches 410; Conservative 210; Mismatches 464; Indels 110; Gaps 38;

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QY 6 ITWAMALLSGFFFPAPASSYNLDVRCARSPSPRAGHFGYRLQV-GNGVIVAGAPE- 63
DB 6 LLLALTLTCHGF-----NLDTEANMTFO--ENMAGFQSGVVOLOGSRVNVGAPBEI 54
QY 64 --GNSGTSLYCCSGTGCHLPVTLR-GSNYTSKYLGMTLATDPDGSILACDPGLSRTCD 120
DB 55 VAAHQRGSLYXOCDSYSGCEPIRLQVPVEAVNMSIGLSLAATSPQLLACGPTVHQCS 114
QY 121 ONTYLSGLCYLFRONLOGPMLQGRPGQECIKG----NVDLVLPDGSMSLQDPBFOKITL 176
DB 115 ENTYVKGICFLFGSNLR---QQPOKPEBARCGCPQSDIAFLIDSGSITIPDFRPMK 170
QY 177 DEMKDVKMLSNTSYQFAVQFSTSYKTEPDPDSDYVKRDPDALIKYKMHMLLTNTFGA 236
DB 171 EFVSTVMEQLKKSNTLPSLMQYSEBFRHFFPKERQNNPNRSLVKPITQLLGRTHTATG 230
QY 237 INYVATEYFEBELGARPATVLLIITDGE--ATDSGNIDAAKD-----IIRYIIGIKH 289
DB 231 IRKVVRBELFNITNGARKNAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDA 290
QY 290 FQTESOETLHKFPASKPASEFVKILDTPEKLDLFTLEOKKIYVIEGSKODLSFNNEL 349
DB 291 FRSEKSRQELNTTISKPPRDHVPQVNNFEALKTIONLREKIFALIEGTQSSSPFERHEM 350
QY 350 SSSGISADLSRGAHVAVGAKDNAGFPLDKADLQDPTFGNEPLTPEVRAGYLGYYVT 409
DB 351 SOEGFSAITNGPLSTVSGSYDNAGVVF-LYTSKEKSTFINMTRVDSMDADATLGVAAA 409
QY 410 WLPBQKTSLLASGAPRYQHMGRVILLFOBPQGGHMSVQTIHTQIGSYGEGELCYDV 469
DB 410 -IIRNRVQSLVTLGAPRYQHIGLVAMFR--ONTGMENANAVKQIGLAVYGASICSVDV 466
QY 470 DQDETELLILGAPLFEVGEORGRVFYI-----ORQUGFEVSHLOQDPYPLGREGEA 524
DB 467 DSNSTDLVTLGAPRYHQIRGQVSVCPPLRGGQAPKQCAV--LYGEQOQWGRFPA 524
QY 525 ITALTIDINGDLVAVAGAPLEE--QGVVYIFNGRHG-GLSPQSORIEGTQVLSGIQWF 581
DB 525 LTVAGDVAGDLTVLVAIGAPBEDNRGAVYFHTGSSGIGISPSHSQRIASGKSLPRQYF 584
QY 582 GRSHGVKDELEGDLAVVAGASOMYVLSRPVVDVMTLMSFSPDAEIPVHEVECSYTS 641
DB 585 GQSSGGGDLTMDGIVLDTVGAQGHVLLRSQPVLRVAKIMEFPRBEVAVRVFECNQVV 644
QY 642 NKMEGVNITTCFOI-KSLYPOF-QGRVAMLTVTLQDGHRTRRGLFPGGRHRLRNI 699
DB 645 -KGEKAGRVYCLHGVKSTRRLRLEGQIQSVVITDLDLDSGRPHSRVAFNETKSTRQOT 703
QY 700 AVT-TSMSCDTPSFHFVPCVODLISPINVSNFSLMBEETPRDQRAQKDIPIILRPSL 758
DB 704 QVLGUTQCEITLKLQLPNCIEDPVSPIVLRNFSL--VGRPLS--ANGN-----LRVYL 753
QY 759 HSEFWETI-----PEPKNGEDKCEANLRVSPSPARSPALMLTAPASISVELSLSNLEED 813
DB 754 AEDQKRFETALPEPKNGCNDNI CODDLISFESFMSLDCLVVGGRBEENVTVTVRANGED 813
QY 814 AYWQOLDLHFPFGSLSPFRVEML---KPHSQIPVSCBELPERSRLSRLL---SCNVSSPI 867
DB 814 SYRQVTFPFFPLDLSYRKVSTLQNKORSORSWRLACES--ASTBVSGLAKTSKCSINPI 871
QY 868 FKAGHVALQMFNTLVNSWGDSEVELTANTYCNNEBDDLLEDSATTI---IPILVYN 924
DB 872 FPENSEVTFNTFPVDSKASLGNKLLAKANTSEN---MPTNKTEFOLELVKAVY 927
QY 925 ILIDQDEBDSITYVFTPKGPKIHQVKMYQVRIQPSIHNDNIPTLEAVVGVPPQSPGPI 984
DB 928 MYVTSHGVTSTKYLNTFASENTSRTVMQYQV---SNIGQSRSLP-ISLIVFLVPLNLQVVI 983
QY 985 THQMSVQMEPPV--PCHYEDLERLPDAAPCLGALLFRCPVY-----1024
DB 984 WDRQVQVTSSENLSTCHTK--ERLPSHD--FLAELRRAPVNCISIAVCORIQCDIPFG 1039

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QY 1025 PROEILVQVITGLTLYGIEBAS-SMPSLCSLSISFNSSKHFLYGSNASL-AQVWAKVD 1082
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QY 1083 VYERKQMLTYVYASIGGGLLLILIFLVLYKVGFPFRNLKKEKBAKRGVNGIIP 1136
DB 1100 PFEVFNPLPIVGVSSVGLLLILITVALYKLGFFPKRYKQYKMMSEG-GPGABP 1152

RESULT 4
RKHUIC
cell surface glycoprotein CD11c precursor - human
N/Alternate names: Leukocyte adhesion receptor p150,95 alpha chain
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C/Accession: A35584; A35543; S00864
R/Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A/Reference number: A35584
A/Contents: extratum
A/Accession: A35584
A/Molecule type: DNA
A/Residues: 1-1163 <COR>
A/Cross-references: UNIPROT:P20702
A/Note: this revision to the sequence from reference A35543 includes the carboxyl end
R/Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A/Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A/Reference number: A35543; MUID:90153906; PMID:2303426
A/Accession: A35543
A/Molecule type: DNA
A/Residues: 1-834 <CO2>
A/Note: this sequence has been revised in reference A35584
R/Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A/Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A/Reference number: S00864; MUID:8816645; PMID:3327687
A/Accession: S00864
A/Molecule type: mRNA
A/Residues: 1-755, '1', 757-1163 <CO3>
A/Cross-references: GB:861695; EMBL:Y00093; NID:g487829; PIDN:AA55180.1; PID:g487830
A/Note: part of this sequence was confirmed by protein sequencing
C/Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on mye
C/Genetics:
A/Gene: GDB:ITGAX; CD11C
A/Cross-references: GDB:119758; OMIM:151510
A/Map position: 16p11.2-16p11.2
C/Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
C/Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
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F/20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F/20-1107/Domain: extracellular #status predicted <EXT>
F/149-319/Domain: von Willebrand factor type A repeat homology <VMA4>
F/1108-1133/Domain: transmembrane #status predicted <TM>
F/1134-1163/Domain: intracellular #status predicted <INT>
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Best Local Similarity 35.0%; Pred. No. 6; e-97;
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QY 12 ALLSGFFFPAPASSYNLDVRCARSPSPRAGHFGYRLQVNGNG-VIVAGAPE---GNSI 67
DB 6 LALLLFTALNTSGFNLDTEELTAFRVDSAG--FGDSVQVYANSWVNVGAPKITYANOT 63
QY 68 GSLYQCSGTGCHLPVTLR-GSNYTSKYLGMTLATDPDGSILACDPGLSRTCDQNTYLS 126
DB 64 GGLYQCSYSGACBEPICLQVPRPAVNMISGLSLASTTSPQLLACGPTVHNEGGRMYLT 123
QY 127 GLCTLFRQNLQGR--MLQGRP-GFQSCIKANVDVLPFLPQSSMSLQDPBPKILDDPKMDVM 163
DB 124 GLCTFL-----GPTQLQRLPVSRQCPROBODIVFLIDSGSISRRNFATMMNFVRAVI 178

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Qy	184	KCLSNSTYCPAAVOFSTSKTEBDSBYKRODPAALLKHYKMLLNTFGAINVATE	243
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Qy	244	VFRBEGADPAKRVLLIITD-----GEATDSNI-----DAKDRIYIGIKHFORKES	295
Db	239	LTHASGARDKATKILLVITDGKGBDSLDYKOVIPMAAA-GIIRIAYIGLAFQRRNS	297
Qy	296	QETLHKFASPKASEPFUKIDTEKLDLTELTELLOKIIYIEGTSKODLTSFMMELSSGIS	355
Db	298	WKEIANDLASKRSEBHI FKVEDPDALQIONQKEIKPAI BEGTTSSSFLEMAQGFSS	357
Qy	356	ADLSRGHAVVGAVGAKDMAGFLDKADLODDTFI GNEPLTPENVAGLYGTYVTMLPSRQ	415
Db	358	AVFPDGPVGLVAGVSSFTWSGAF-LYPPMWSPTPI NMGENVMDRSDYIGYS-TELAMWK	415
Qy	416	KTSLIASGARVYQHMGRVILLPOEPPQGGHWSOVQTHGTQIGSYRGSELCAVDYDQGET	475
Db	416	GVOSLVLAGARVYHTKAVIF--TVQSRQMRKBAVETQIGSYFGASLCVADVDTGST	473
Qy	476	ELDLIGAPLYEGGEORGVFIYOR-----ROLFBESELEODPPGLCPFEALATLTDI	531
Db	474	DLVLIGAPHYTEQTRGGQVSVCLPRGMRRMWCDAV--LYEGQGHMKRFPALATYIGDV	531
Qy	532	NGDGLVDVAVGAPLEBO--GAVYIFNGRHG-GLSPQPSORIEGTQVLSGLQMPGRSHGV	588
Db	532	NGDMLTDVVI GAVGEENAGAVYLFHGVLPGISPSHSGRLAGSGLSRGLYFQALSGG	591
Qy	589	KDJBEGDLADVAGASQMI VLSRPVDMTILMSFSPAEIPIVHEVBCSYSTSKMKEGV	648
Db	592	QDLPQOGLVDLAVGARGQVLLRLTRPVLVWGVSMQFIPAEIIPRSAFECREQVVSER-OTLV	650
Qy	649	NITICPQIKSLYPOQGR--IVANLYTLQDLGHTRRRGJ.FPRGRH-ELBRNIAVYTM	705
Db	651	QSNICLYIDKRKSNLLGSRDLOSSVLDLADLPGLSPRATFOETKNSLSRVAVLILKA	710
Qy	706	SCDPSFHFVPCYODLISPINVSINLSMEEBEGTRDROAOGKOIPI--LRPELSER--	761
Db	711	HCHRNILLPSCYBEDSVTPITLARINTL-----VCKPLAARNLRPMLADAQ	758
Qy	762	---TWELIPFEKNCGEDKCCENLRVSPSPARSALRLTAFASLSEYLSLSNLEBDAYWQ	818
Db	759	RYEFLASLPFEKNCGADHICODNIGISFSPGLKSLVGSNLENAEVMVMDGEDSYGTT	818
Qy	819	LDIHPFPGLSFKRYEMLKPHSQ---LPSCELSPEESRLLSRALSCNVSSPIFPAQHSVA	875
Db	819	ITESHHPAGLSYRVVABGQOQLRSJLHLCDSAPVGSQ-GTWSITSCTRINHILIFRGAQIT	877
Qy	876	LQWFMNVLVMSWGSDELHANTCNNEBSDLLEONSATTI---IPLIYINILIQOED	932
Db	878	FLAIFEDVSPRAVLGDRLLLTANVSENN---TPRTSKTTQLELPVKIAYTVVSSHEQ	933
Qy	933	STUVJSETPKGPK-IHQVKMYQVRLQPSIHDHNIPT-----LEAVGV	975
Db	934	FTKYNINSEBEKESHVAMHRQVN--NLGQRDLPVGINFVPELVNQEAVMMDVESH	990
Qy	976	POPSBGPITHQMSVOMEPVPCHEDLERLPDAABPCLPAL-FCRCV--VFRQELV	103
Db	991	POHNS---LRCSSEKIAPPASDPLAHIOKN-VLDCSIAGCLFRCDVPSFSVOEELDF	104
Qy	1032	QVIGTLEL--VGEIEMASMPSLCSSLSISFNSKHFIHLYGSNALSIAQVVMVVDVVEKOM	108
Db	1046	TLKSNUSFGWNRQI-LQKXSVSVSAIEITFDYSVSQLPQDBAFRR--ADTTVLEKYK	110
Qy	1090	LY-----LYVLSGIGGLLLLLLFIYLYKVGFPRKMLKEKMEKGRG--VPNG--IPAEBS	114
Db	1102	VHNPPTLIVGSSIGGLLLALLATLTAVALYKVGPFKQYKEMMEBANQAIAPENGQTPSPPS	116
Qy	1141	EQ 1142	
Db	1162	EK 1163	

RESULT 5  
S00551  
leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse  
N.Alternate names: complement-3 receptor alpha chain  
C.Species: Mus musculus (house mouse)  
C.Date: 30-Sep-1989 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C.Accession: S00551, I59078  
R.Pyrcella, R.  
EMBO J. 7, 1371-1378, 1988  
A.Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the i  
A.Reference number: S00551; MUID:8832584; PMID:3044779  
A.Accession: S00551  
A.Molecule type: DNA  
A.Residues: 1-1153 <P>  
A.Cross-references: UNIPROT:P0555; EMBL:X07640; NID:952982; PIND:CAA30479.1; PID:952983  
A.Note: the authors translated the codon CAC for residue 569 as Gln  
R.Saetre, L.; Roman, J.M.; Teplov, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,  
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986  
A.Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep  
A.Reference number: I59078; MUID:86287312; PMID:2942940  
A.Accession: I59078  
A.Status: preliminary; translated from GB/EMBL/DBD  
A.Molecule type: DNA  
A.Residues: 11-44 <RSS>  
A.Cross-references: GB:M14293; NID:g198993; PIND:AAA39484.1; PID:9554193  
C.Genetics:  
A.Gene: Mac-1  
A.Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo  
C.Keywords: cell adhesion; glycoprotein; transmembrane protein  
F.I1-16/Domain: signal sequence #status predicted <Sig>  
F.I17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental  
F.I148-318/Domain: von Willebrand factor type A repeat homology <VWA2>  
F.I1106-1129/Domain: transmembrane #status predicted <TM>

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QY	ITVMMALMLSGFFFPFAPASAYLVDVRGARSFSPBPAGHFGYRVLYQV-GNGYIVGAPGEG	64		
DB	6 LITVLMALCHGF-----NLDIEHMTQENAKG--FGQNVVLGGTSIVVAAPQEA	54		
QY	65 --NSTGSLVOCOSGCTGHCLPVTLR-GSNYSKYLGMTLADPTDGSILADCPGSLRTCD	120		
DB	55 KAVNQGTALYQODVSTRCHPIQLVPPBAVMMSGLSLAVSTVPQQLLAGCPYHQNCK	114		
QY	121 QNTYISGLCYLFRONTLQGMLOGMRPOECLKANDVLVFLDGSMSLQDPEFOKLIDPMK	180		
DB	115 ENTYYVNGLCYLFSGSNILRRPQOFPREALRECPQESDIDVFLIDGSGSINNIDFQKMKFVS	174		
QY	181 DVMKLTSTYSQFAAVQFSTSKTEFSDSDYVKRDPDLALKVYGHMLLTPTTPGALNV	240		
DB	175 TYMEQFKKSKTFLFSLMQYSDFERLHFTFNDFGRNPSPSHVSPIQLNGRTYTAAGIRKY	234		
QY	241 ATEVREELGARPDAITKVLIITDSE---ATDSENIAAKD---IIRYIIGIKHFQTK	293		
DB	235 VRELPHKNGARENAKILVVIITDDEKCGDPLDYQDVLPBADRAVGIKVIIGVNAFNKP	294		
QY	294 ESQETLHFPASKPASEFYKILDTPEKLDLFTLEQKILVIBGTSKODLTSFNMELSSSG	353		
DB	295 QSRRELDTASKRPAGEHVFQYDNFALNTIINQOLDEKIFALIGTQSTSFSEHMSQEG	354		
QY	354 ISADLSRGHVAVVGAGADWAGG-FLDKADLQDPTFIGNEBLTEVNAAGYIGYIVTLP	412		
DB	355 FSASTSTNGPLIGSGSFDWAGGALYTSKD--KYTFINTRTVDDMDMDAYIGVAYSAVI-	411		
QY	413 SROKTSILASGAPRVOHMGKRVLLFQEPQCGGMSQVOTIHGQIYSFGESLGGVDVDD	472		
DB	412 LRNRQSLVLGAPRQIGLGYVMPRE--NFGVMHEHTSIKSGQISYFGASLCSVDMMD	469		
QY	473 GETBLLILGAPLFGEORGRVFI--YORORLGFEEVSELOQDPGYPLGRFGEAITALTD	530		
DB	470 GNTNMLILGAPHYEKTGGGVVCPPLPRGRAPRMCBMLLHDDQAHPMGRFPAALLTVLGD	529		

Qy	26	INLWYRGARSGSPRAGHREYRLQY-----GNCVITYGAGEG---NSTSIVYOCOSGTC	78
Db	1	FNVIDKSNMTSGP-VEDMFGYTVQYENEBGKVVLLGSLVQGPARRDVTYVCKPVGRC	59
Qy	79	HCLP-----VTLRGSNYISKYLGMLATDPTDGSILACDPGLSRFCDOPTY	124
Db	60	ESLPCVUKDLFVNYSIPNVTBVKNNM---FGSLVTINP--NGGFLAGPLIYARCGHLHY	115
Qy	125	LSGLCYLFRNULOGRPMLOGRPFQECIKGNVDVLFPLDGSNSLOPDEFQKILDPMKDVMK	184
Db	116	TYGICSDSPFFQ--VWNSIAPVOEC-STOLDIYIVLDGSNSIYIP--WDSVTAFLNDLTK	170
Qy	185	K--LSNTSYOAAVOFSTSYKTEDEPDSGYARKOP-DALLKHYVMMLLNTTGAIVYA	241
Db	171	RMDIGPKOTQYIYOYGENVTHEENLNKISTEVELVAAKKIYORGRQTMALGDTAR	230
Qy	242	TEVFEELGAPADATKVLIIITDEATDGSNIDAA-----KOIRYIIGI-GKH-----F	290
Db	221	KEAFTEANGARGYKXWVIVLTDESHDNHRLKVIODCEBENIQRSAIILSGYNNGL	290
Qy	291	QTKESQETLHKPASKPASE-FVKILDFEKLKOLFTELQKKIYVBGTSKQDLTSPMEL	349
Db	291	STEKVEEIKSIASEPEKHFENVSDEI-ALVITVKIGERIFALFATAOQSAASFEMEM	349
Qy	350	SSGSIASLISGHAVGAVGAKMAAGFLODKADL-----ODDPF-----IGNEPLPEVR	400
Db	350	SQTSASAYSODMWLGAVDMNGVNVQKASQIIIPRTTFNVSTKKNBEL-----	404
Qy	401	AGYLGYYTWMPSRKQTSILASGAPRYOHMGRVLLFQEPQGGHMSQVQTHGTQISYF	460
Db	405	ASYLGYTNSMTASSGDVLIIAAGPRNHTQGVITR--MEDGNIKILOTLSEQIGSYF	462
Qy	461	GGEICGVVDODGESTELLIGAPLYG--BORGRAVITYOROLOGFEVESELQ-----	511
Db	463	GSILTTDIDXDSNTDILVGAPMYMEKEBEQKVYVYALNQTRFQYMSLEBIKOTCC	522
Qy	512	-----GDPPYLG-RFGEAITLTLTDINGGLVDVAVGAPLEQ--GAVYIFNGRH	558
Db	523	SSRQNSCTTENKNEPCGARGPITLAAVKDNLDFNDIYIAGLEDDHGCAVYIYHSG	582
Qy	559	GLASPOPSQRIEQTQVLSGIOWFGRSIGHVQDLEBGDLADVAVGABSOMTILSRPVDM	618
Db	563	KTIREXVQRIPSGGDDKTLKFFQGSIHGEDMNDGDLVTYIGLGGAALFMSRDVAV	642
Qy	619	VTLMSFSAELPHEVBCSYSTSNAKKEGVNITTCFQIK-----SLYPOQRHVAUNT	672
Db	643	KVTNMFENKNVNIQKNC--HMEKEITVCINATVCFEYVUKSKSKEDITYE-----ADLQ	693
Qy	673	YTLQDGHRTRRRGLPQGR-HELKRNIAVTTSMCDFSPHFVPCVQODLISPINLYNF	731
Db	694	YRVTLDSLRQISRFSTQERKQORNIYWRKS-ECTKHSFTM-LDGHDPQDSVRIITLDF	751
Qy	732	SLMEEBGTPRQARQOKDIPILRPSLHSETWE-IPEKNGCGEDKCKEAMLRVSPARS	790
Db	752	NLTLPEN-----GPVLDDSLPNSVHEXITIPAKOXNNKEKISDLSLHVATEK	799
Qy	791	PALRL-TAPASLVELSLSNEEDAYVQDLAEPPGLSTRKYMALKPHQOIPYSGELP	849
Db	800	DLLIYRSQNDKFNVSLTVKNTKQSAVYTRITVHSPMLVFSGEIAIOKD-----SCES--	852
Qy	850	ESRSLSLAALSVCNSPFIKAGSHVALOMMENTLVNSW-GDSVEHLANTYCNNE--SDL	907
Db	853	-----NNNTCKQGYPLRKGEMVTKLIFQ--FNTSYLMENTVITYLATSDBEEPET	904
Qy	908	LEDSNATITILYLPINI-LIODQEDSTLYVSPKPKKI-----HOVKHMYQVRIQ	958
Db	905	LSDNVMSISIVKTEVGLOFYSSASEXHISIAANETVPEVINSEDIGNEINIFYLIRS	964
Qy	959	PSIHDMNITLEAVAVGPQPSBG-PITTHQMSVOMEPPVCH--YEDL-----EFLPD	1008
Db	965	GSF--PMPELKLKISIPNMTNSNGYPIVLYPTGLSSSENACRPHIFEDPDSINSKGKMTT	1021

Db 1022 STDHLKRTTIDCNCCKPATTCNL- -TSSDISQVNVSLILMKPTFKISYFSSLNTLRG 1079

Qy 1062 SKHFPLYSNANSLA-----QVWKVQVNVVEKQMLYLVYSGILGILLIFVL 1111

Db 1080 ----ELREBNASVLSSNQKRELAIQISDGLPERVNLWILSLAPAGILLMLIAL 1135

Qy 1112 YKVGFFKRNLEKME 1126

Db 1136 WKIGFFKKPLKKME 1150

RESULT 7

A35854

Integrin alpha-1 chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 23-Oct-1990 #sequence\_revision 13-Sep-1991 #text\_change 09-Jul-2004

C:Accession: A35854; S11243

R:Rignattus, M.V.; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonetto, J. Cell Biol. 111, 709-720, 1990

A:Title: Molecular cloning of the rat integrin alpha-1-subunit: a receptor for laminin a

A:Reference number: A35854; MUID:90338125; PMID:2380249

A:Accession: A35854

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-1180 <INP>

A:Cross-references: UNIPROT: P18614; GB:X52140; NID:956493; PIDN:CAA36384.1; PID:956494

C:Keywords: cell adhesion; cytoskeleton; transmembrane protein

F:1170-345/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 18.2%; Score 1112.5; DB 2; Length 1180;

Best Local Similarity 27.9%; Pred. No.2.9e-68;

Matches 351; Conservative 221; Mismatches 457; Indels 231; Gaps 52;

Qy 4 SCITTMAMALISGFFFAFPASSYNDVFGARSPSPRAGRHFGRVLYQ---GNGYIVG 59

Db 14 ACIMVLITVIL--GF-----CVSFNDVAKNSMSFSGP-VEDMFGYVVOQYENEBEKWYLIG 65

Qy 60 APDEGN---STGSLYQCGSGTGHCIP-----VTLKGSNTSKYLGMLTLATD 102

Db 66 SPLVQCPARPTGVDYKCPVGRBRAPCVKLDLPNTSLPNTVEIKENNT--FESTLVTN 122

Qy 103 PTDSIILACDPGLSRTCDONTYLSGLCYLFRONTLOSPMLQGRPGFQECIKGNVDLFLFD 162

Db 123 P-NGGFELACGPLVYARCGHLHYTTGICSDVPTPQ--VNVSPAPVQEC-STQGLDIVLVD 178

Qy 163 GSNGLQDPBEFKILDFMKDVMKK--LSNTSYQPAAVQFSTSYKTEPFDSYVKKRDPDL 220

Db 179 GSNSTYF--WESVIAFLNDLLKRMIDGPKQTVGVIGENVTBHFNLNKY----- 227

Qy 221 LKHVGMILLNTRG-----AINVATVYFRELGRARDATVLLITIDGERTD 269

Db 228 -SYTEEVIAVNAKLGROGGLQTMALGIDTPARKKAFLEARARARGVKKVMVITVDGESH 286

Qy 270 SGNIDAA-----KDIIRYIIGIGKGF-----QTESQETLHKASKPRASE-FKILIDTF 317

Db 287 NYRLKQVYQDCEDENIQFSTAILGHYNRKGLSTBKFPYEBIKSLASBETGHHFNVDEL 346

Qy 318 EKLKDLFTELQKIVIEIGTSKODLTSPFMELSSSGISADLSRGAHVAVGAVGADWAGGF 377

Db 347 -ALVTIVKALGERIPALBATDQSAASPEMMSGQGFSAHYSQDMVMLGAVGADVMNGTV 405

Qy 378 LDKYKD-----LQDDTFIGNREPLTPERAGILGTVV--TWLPSQKTSLSLASAPR 426

Db 406 VMQKRNQVVIPIHNTTFQTEPAKMEPL-----ASTLGATVVASATIPG---DIVLIAQPR 457

Qy 427 YQHMGRVLLFQEPQGGHMSQVOTIHGTQISYFSGELCGVDVDDGETELLILGALFLY 486

Db 458 YNHGQGVVIYK--MEDGNINILQTLGSRQISYSGTSVYTTTIDDKDSTDLLVIGAMVM 515

Qy 487 G--EORGRVRFYQRRQLGFEEVSELQ-----GDPGYPLVG-RFEGAIT 526

Db 516 GTEKEQCKVVYVAVNQRRFQWMSLEPIRQCCSSLLKDNCKTENKNEPFGAAGFGTALA 575

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QY      527 ALTDINGDGLVDVAVGAPLEBQ--GAVYINGRHGGISLPDSQSIIEGVLSIGIOMFGRS   584
DB      576 AYKDLIVDFENVDNVIAPLEDHDAGAVYIYGSGKTIIEAYQRIPSGDGDKTLKFPGQS   635
QY      585 HGVVDLJEDGDADVAVGAESQMVLVSRRPYMDVTMTSPSPAIPIVEEVCYSTSNM    644
DB      636 HGEBDINDGDLTDTVTITGIGGAALFARADVAVKTMNEPKNVIOKKNC--RVEGKE   693
QY      645 KEGVNITICFOIK-----SLYPFOGRLVANITYTLQDGHRTTRRRLPFQGR-HELR   697
DB      694 TWCINATWCFHVHLKSKEDSIVE-----ADQLQRYVLDSLRFQISRFFSGTGQRKIQR   746
QY      698 NIAVTTSMGCTDPSHFPPCVODLISPINSINSPSLMEEBETPRPDQRAQKDIPILARS   757
DB      747 NTTVRES-BCIRHSFTM-LDKHDPDSVRVLTFLDNLDPEN-----GVLDDA       792
QY      758 LHSETWE-IPEKNCGEDKKCBANLRVSPSPA-RSRALRLTAPASLVSELSLNDEDAY   815
DB      793 LENSVEHEIIPKADCCNKERCISDLTLNVSTTERKSLLIYVSQHDKFNVLTYKKGDSAY   852
QY      816 WVOLDHFPFGISFRKYEMLKPHSQIPVSCBELPEBSRLLSRALCNVNSPFIKAGHSA   875
DB      853 MNRIVVQHSPLNIFSGIEBIQKD-----SCES-----NQNTICRGVFPLRAGEYTV   899
QY      876 LQMM-FNTLVNSSWDSDVELHANVTCNNEDS-DLEDNSATTIIPIIYIPNI-LIQOE   931
DB      900 FFIHQFNT---SHUSENAIHLSATSDEEPLESINDNEVNISIPLYCEVGLDQFSAS   956
QY      932 DSTLYVSPFKPGKI-----HOVMHWQVRIOPSIDHNIPTLEAVGVOPQPSBG-   982
DB      957 EHHISVANETIPEFINSTBEDIGNETINVFTYTKRGHP---PMELQGISIPPMLTADGY   1013
QY      983 PTHQMSVQMEBPVPCHYEDLE-----RLPDAEPC-----                  1013
DB      1014 PLYLPIGWSSNDNVNCRPSLBDFPGINSCKMTISKBVLKRGTIQDCSSTCGVATITC   1073
QY      1014 --LPGALRFCPV--VPROEILVQVIGTELEV-GELBASMFSLCSLSISFNSSKIFH   1066
DB      1074 SLIPDLSGVNVSVLLMKRPTFIKAHPSNLTLRGKEKSEN-----SSLTSSSKRK--   1126
QY      1067 IYGSNASLAQVMKVVVVEKOMLYLVLSGIGLLILLFIYLKYKGFPEKNIKEME   1126
DB      1127 -----ELAIOISK-DGLGRVPLMWILLISAPACGLLMLLMLLIMLKIGFFKRPKKGME   1179

RESULT 8
145914
Integrin alpha 2 subunit - bovine (fragment)
C|Species: Bos primigenius taurus (cattle)
C|Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C|Accession: I45914
R; Kamata, T.; Puzon, W.; Takada, Y.
J. Biol. Chem. 269, 9659-9663, 1994
A|Title: Identification of putative ligand binding sites within the I-domain of integrin
A|Reference number: A54402; MID:94193647; PMID:7511592
A|Accession: I45914
A|Status: preliminary; translated from GB/EMBL/DDBJ
A|Molecule type: mRNA
A|Residues: 1-1170 <KAM>
A|Cross-references: UNIPROT:P53710; GB:I25886; NID:g439695; PIDN:AAB59255.1; PID:g439696
F|61-336/Domain: von Willebrand factor type A repeat homology <vMA2>

Query Match          16.6%; Score 1012.5; DB 2; Length 1170;
Best Local Similarity 28.2%; Pred. No. 2, e-61;
Matches 346; Conservative 209; Mismatches 459; Indels 211; Gaps 56;

QY      25 SYNLDRGARSSPPRAGHPGRLVQV-----GNGVVGAPGEG---NSTSLYOOC--QS   75
DB      18 ANNGVLPRAKTISGP-SSEQGTAVOOFINPKGNWLVLVGSFWSCFPKKRMGDVTKCPVDL   76
QY      76 GTGHCPLPVLARGSN-----YTSKYLGMTLATDPTDGSILACDPGLSRTCDONTYLSG   127

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Db      77 STTCEKINLQSTSMNVTEKTNMSLGLTLTRNVGTGFLTCGPMLAQQCGSQYTTG 136
Oy      128 LCYLFRONIQ-----GPMLOGRPGFQECIKGNVDLVPFLPDGSMSLQDPDFKILDPMDV 182
Db      137 VCSDVSPFOARTSPAPAVQTCPSF-----IDVVVCDSENSTYF-----MDAVKNF 183
Oy      183 MKK-----LSNTSYQFAAVQFSTSYKTEPDFSDYKRKDDPALKHVKHML-----LTN 232
Db      184 LEKFQGLDIPRTKQMLIQVANNPRVFNLMNPF---KSDENMKANSQTFQYQGDLTN 240
Oy      233 TFGAINVYATEVREBELGAPDATVLIITDGEATDSGNIDAAD-----IIRYITGI 286
Db      241 TPKAIQVARDYATPAAGRPGATKTVWVVVDGSHSDSKAKAVDQCCKNUNILRFGLAV 300
Oy      287 -----GKHFOTKESQETLHKFASKRPS-EPFKILDPTEFKDLDFELQKTIYVIEGSKQ 340
Db      301 LGYLNRLADTKNLKEIKALIASLPTENHFRVSDADLEKAGT-IOEQIFSLBGT-VQ 358
Oy      341 DLTSFNNMELSSSGISADLSRGHAV--VGAAGAKWAGGFLDLKADLDQDTEIGNEP--- 394
Db      359 GGDNFQWEMSGVGFSAEYSPQNNILMLGAVGAYDMSG-----TVVQKTPHGL 406
Oy      395 -----LTPEVAGIYLYTWTMLPSRQKTSILASGARYQMGVLLPQEPQGGH 444
Db      407 IFSKQAFQIILQDRNHSSYLGSVASISTGNSVHFVA-GAPRANTYQIIVLYSVNE-NGN 464
Oy      445 MSQVOTIHTQIGSYFGELCGVDVDQDETLLIGAPLFYGE--QRGGRVITY--QR 500
Db      465 VTIVQSQMGDQIGSYFGSVLCANDVNKOTITDVLVGAQPMWMDLKEBGRVYLFITKG 524
Oy      501 QLGFEVSELOQDPGYPLGRFGEAITALTIDINGDLVDVAVGAPLEEQ--GAVYIFNGRH 558
Db      525 ILNMHQF--LEBPGMLENARFGSALIALSDINMDGFNDVIVGSPLENQSGAVYIYNHGE 582
Oy      559 GGLSPQSPQREBGT--VLSGIQWFGRSIRHVKYLEBGLADVAVGAESQMTIVLSRPV 616
Db      583 GMILRYSQKILGSRAPASHLQYFGRSLDYGDLNGSITDVSVGAGQVQVWLSQSLA 642
Oy      617 DMVTLMSFSPAPIPVHEVCSYSTSNMKKEGVNITICFOISLYQFQGRLVANLTYLQ 676
Db      643 DVSVDASTTPKTI-----TLANKAE-IKLKCCTSAK-FRPTNNONVA-IVNYIT 690
Oy      677 LD-----GHTRRKGLFPGGRHE-LRNIAVTTSMSCDTFSFHPVYQVDLISPINVSLNF 731
Db      691 IDEQFSSRIVSRGLFKENNERCLOKTMIVQAOQCSYIIHIGE-PEDIIISPLMCNI 749
Oy      732 SLMBEGTTPROQRAQKDIPIRLPSTL-HSET--WEIPFKNGEDKCBAN-LRVS 784
Db      750 SL-ENPGT-----NPALEAYSEYVVFISIPFKKCGDGDGVCISDLVINVQ 793
Oy      785 FSPARSLRLTLAFAS--LSVELLSNLEEDAYWQDLHFRPGLSFPKXVEMLPHSQIP 842
Db      794 QLPATQOQPIVSNONKRLTFSVOLKMKESAHYTEIVVDSSENLFFFSMSGM-----P 846
Oy      843 VSCBELPEBSRLSRALSCNVSPIFKAGHSVALQMMEN-TLVVSSWGDSEYELHANYTCN 901
Db      847 VDGFEVTCQIASSQGSYTCNVGYPALKSKQCVTFINDFMLQNLQNGASISFPA---LS 903
Oy      902 NEDDLLEDNATTIPIILYPINILIQ-----DOBSTLYVSPFKPKPKIHQV 949
Db      904 ESOBENMADNSVNLKSLLYDAEIHITRSTININFEVSLDGNVSSVHVSFEDIGPKF--- 960
Oy      950 KHMTOVRIOPSIHINIPTLEA--VVGVPQ--PSPSGPITHQMSVQMBE--PVPCGYE--D 1002
Db      961 --ISIKYTTG--SVVSMASVYIHIPOYTKDKNPLMYLTGHTTDAAGISCBAIINP 1014
Oy      1003 LERLPDAEPLCPGALFR-----CPVVFROEIL-----VOYIGTLEL-----VGEIE 1044
Db      1015 LKIGQTSSTSVSFKSENFHAIKELNCRTASCNIMQWLDLQVKGEPYLVNSTRIMNGFA 1074
Oy      1045 ASSM--PSLCSLSISFNSKGFHLYGSNADLAOVNKKVDVYVEKQMLYLYLGG--IGG 1100
Db      1075 ASTQTVQTLAAAEIDTYNPQIYVIEBNTVTIPLTIK--PHEKEVPTQVIVGSYIAG 1131

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Oy      1101 LLLLLIFIVLYKVFPRMLKEKM 1125
Db      1132 ILLLLALVALIMKLGFPRKRY-EKM 1155

RESULT 9
A:33998
N:Alternate names: CD49b; platelet glycoprotein GPIa; VLA-2/collagen receptor alpha-2 ch
C:Species: Homo sapiens (man)
C:Date: 30-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 09-Jul-2004
C:Accession: A33998; B56793; A53117
R:Takada, Y.; Hemler, M.E.
J:Cell Biol. 109, 397-407, 1989
A:Title: The primary structure of the VLA-2/collagen receptor alpha(2)-subunit (platelet
A:Reference number: A33998; MUID:89308879; PMID:2545729
A:Accession: A33998
A:Molecule type: mRNA
A:Residues: 1-1181 <TAK>
A:Note: the authors translated the codon GAT for residue 802 as Gln, GTC for residue 803
R:Catalini, B.; Parmentier, S.; Leung, L.L.; McGee, J.L.
Biochem. J. 279, 419-425, 1991
A:Title: Separation of important new platelet glycoproteins (GPIa, GPIC, GPIC*, GPIIa and
A:Reference number: A56793; MUID:92061944; PMID:1953640
A:Accession: B56793
A:Molecule type: protein
A:Residues: 30-43 <CAT>
A:Experimental source: platelet
R:Zutter, M.M.; Santoro, S.A.; Painter, A.S.; Tsung, Y.L.; Gafford, A.
J. Biol. Chem. 269, 463-469, 1994
A:Title: The human alpha-2 integrin gene promoter. Identification of positive and negativ
A:Reference number: A53117; MUID:94103255; PMID:8276836
A:Accession: A53117
A:Molecule type: DNA
A:Residues: 1-16, 'V', 18-21 <ZUT>
A:Note: references: GB:L24121; NID:9400342; PIDN:AAAL619.2; PID:94583535
C:Genetics:
A:Gene: GDB:ITGA2; CD49B
A:Cross-references: GDB:128031; OMIM:192974
A:Map position: 5q11.1-5q11.2
C:Keywords: cell adhesion; glycoprotein; heterodimer; transmembrane protein
F:1-29/Domin: signal sequence #status predicted <SIG>
F:30-1133/Domin: extracellular #status predicted <EXT>
F:1134-1154/Domin: transmembrane #status predicted <TM>
F:1155-1181/Domin: intracellular #status predicted <CYT>
F:105,112,343,432,460,475,699,1057,1074,1081/Binding site: carbohydrate (Asn) (covalent)

Query Match 16.1%; Score 985; DB 2; Length 1181;
Best Local Similarity 27.6%; Pred. No. 1,9e-59;
Matches 349; Conservative 210; Mismatches 484; Indels 220; Gaps 54;

Oy      8 VMAMALLSGFFFPAPASSYNLDVGRSFPAPRGRFGYRVQV-----GNGYIVGAPGE 63
Db      14 LVVIALSQGLNCLLA--YVVGLPKAKIFSGP--SSQFGYAVQGFINKPKNMILLVGSFWS 70
Oy      64 G---NSTGSLYQC--QSGTGHCLPVTLRGSN-----YTSKYLQMTLATAPTDGSILA 110
Db      71 GFPENRMGDVYKCPVDLSTACEKMLQTSISIPNTEKMTNMSLGLILTRNMGTGGLTF 130
Oy      111 CDRELSTTCQNTYLSGLCYLFRONQO-----GPMLOGRPGFQECIKGNVDLVPFLPDGSM 165
Db      131 CGPLMAQQCGNQYTTGVCSDISPDQLSASFPAQPCSTL-----IDVVVCDSEN 183
Oy      166 SLOPDEFQKILDPMDKVMKK-----LSNTSYQFAAVQFSTSYKTEPDFSDYKRXKDPDA 219
Db      184 SIYP-----WDVAKNLEKFFVQGLDIPKTVGLIQVANNPRVFNLMNPF----- 229
Oy      220 LKHKVKMLL-----LNTFGAINVYATEVREBELGAPDATVLIITDGEAT 268

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Db 230 --KTEEMIVATSTQSYGCDLTNTFGAIQVARKTAYASAGRRSARFKVWVVTGDSH 287
Qy 269 DSGNDAAKD-----IIRYIIGI-----GKHFQKESSETLHKRASPASE-FKILDT 316
Db 288 DSGMLKAVIDQCNHNDILFGLAVAGYLRNALDITKMLKEIKALASIPTEBYFFNVADSE 347
Qy 317 FEKLKDLFTELQKTIYVLEGTSCODLTSPFMELSSSGISADISRGHAY--VGAVAKOMA 374
Db 348 AALLERKAGT-LGEOJFSIEGT-VGGDNFQEMMSOVGSADISSQNDIMLGAVAFGWS 405
Qy 375 G-----GFLDLKADLDODTFIGNEPITPEVRAGYLGYYTWLPSRKSTSLASGAR 426
Db 406 GTIVQKTSHGHLIPKQAFD-----QILDQNHSSYLGYSVAALSTGESHTFVA-GAPR 458
Qy 427 YOHMRVLLFOEPQGGGMSQVQTHGTQIGSYFGSELGVVDVDDGETELLITAPLFY 486
Db 459 ANYTCQIVLYSVNE-NGNITVVIQARHGDIQSGFSVCSVVDVDDTITDVLVGAPEWM 517
Qy 487 GE--ORGGRVFIYORRQGLGFEVSHLOQDPGYPLGRPGBATLTDINDGGLVDAVAP 544
Db 518 SDUKKEBGRVYLFTTKGILGHOFLGEPGEGIENTRFSALALSDINDGDNVIVGSP 577
Qy 545 LEBQ--GAVYLFNGRHGGLSPQSORIEGTQ--VLSGIQWFGRSIHGVNLEGGDLADVA 600
Db 578 LENQSGAVYIYNHOGTIRTKYSQKILGSDGAPRSHLQYFGRSLDGYGLDNGSDITDVS 637
Qy 601 VGASEQMTVLSRPVVDVNTLMSFSPALIPVHEVECSYSTSNKKEGVNITTCFOIKSLY 660
Db 638 IGAFQVQVQVLMQSIADVAIEASFPEKTI-----TLVKNQAQ--ILKLCFSAK-FR 686
Qy 661 PQFOGRVLANLYTTLQD-----GHTRRRGLFPGGRH-IRRNIAVTSMGSTDSPHFP 715
Db 687 PKQNNQVA-IYNNITLADGSSSVTSRSGLEKENNERCLQNMVWVNAQSCPEHITIQ 745
Qy 716 VCVQDLSPINVLNFSLMEEBGTPRDQRAQKDIPIILPSEL-HSET--WELPPEKN 770
Db 746 E-PSLVVNSLDLRVVISL-ENPQT-----SPALBAYSETAKYFSIPIFKD 788
Qy 771 CGBKKCEAN--LRVSPSPARSRLRLTAAPS--LSVELSLNLEEDAYWQDLAHPFG 826
Db 789 CGHDELCTISDLVDVROQIPAAQOEPIVSNQKRLLTFSVTLKNKESAVNTGIYVDFSEN 848
Qy 827 LSFRTVEMLKPHSQIPVSCBELPESRLLSRALSCNVSSEPIFKASHVALQMKR-TLVN 885
Db 849 LFPASF-----SLPVDGTEVTQVVAASQKSVACDVGYPALKRQOVTFTINFENQON 901
Qy 886 SSMGDSVEIHAHVNTCNNESSLLEDNSAFTIIPILYPINI-----LIQDQSDS 933
Db 902 LQNKASLSFQALSESQEBK--ADNLVNLKIPLYDAEIHILTRSTNINFEISSDGNP 958
Qy 934 TLVYSPFKPKIHOVKHMYOVRIOPIJHDNIPTLEA--VWVGPQPPSE-GRITHQMSV 990
Db 959 SILVHSEFEDVGRKF-----IFSLKVTG--SVPSMAVTIIHIOYKTEKNPLMYLGV 1009
Qy 991 QMEP--PVPCC-----HYEDLEKLPDAEELCPALFRCPVVERQ 1027
Db 1010 QTDKAGDISCANINPLKIGOTSSSVSPKSENFRTKELNCRTPASCNVTCMLKDVHMKG 1069
Qy 1028 ELVVOVIGTLBELVGEIASSMF---SLCSSLSISNNSKHPLYSNMSLQOVWKKVUV 1084
Db 1070 EYFVAV--TTRIMNCTFASSTFTQVQLTAABEININVEIYIENVTYIPLMKRP-- 1125
Qy 1085 YEKQMLYLYVLSG--IGGLLLLLLIYLYKVGPKRMKEKMEAGRGVPGNIPRADEBQ 1142
Db 1126 -EKAEPVGVIGISIIAGILLALLVALIMKLGFPRKY-EKM-----TKNPDEIDETTE 1178
Qy 1143 LAG 1145
Db 1179 LSS 1181

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integrin alpha-E chain - human
C.Species: Homo sapiens (man)
C.Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C.Accession: A53213
R.Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A.Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. Un
A.Reference number: A53213; MUID:94164962; PMID:8119947
A.Accession: A53213
A.Status: preliminary
A.Molecule type: mRNA
A.References: 1-1179 <SHA>
A.Cross-references: UNIPROT:P36570; GB:L25851; NID:g457244; PID:g457245
C.Genetics:
A.Gene: GDB:ITGAE
A.Cross-references: GDB:330801
A.Map position: 17p13
C.Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo
F.199-371/Domains: von Willebrand factor type A repeat homology <YMA3>

Query Match 16.0%; Score 976.5; DB 2; Length 1179;
Best local Similarity 26.0%; Pred. No. 7.5e-59;
Matches 330; Conservative 214; Mismatches 454; Indels 273; Gaps 47;

Qy 6 ITWAMMLSGFFFAASSYNDVRGARSPPRAGRHPGYRL-----QVNGVTVG 59
Db 8 LCISALALAAV-----NVDV--ARPWLTGKGAAPVLSLHQDPSTNQTWLLVT 56
Qy 60 APGSGNSGLYQCSQNGH--CLPV-----TLRGSNTSKYLGTLATDPDGSILACDP 113
Db 57 SPKRKRTGRLRSLVODDELCHPVEHVPKPK-----RRKGVTVARS-HHGVLICQV 110
Qy 114 GLSFTCDQNTYLSGLCYLFRONTQGPML--QGRDPF----- 147
Db 111 LVRRPHSLSSLTGTC-----SLGPDLRPQAQNFDEVLDPDARVDTGDCYSNKEG 165
Qy 148 -----QECIKGNVDLVFLPDSMSLQRPBFQKIDFM 179
Db 166 GGEDVNTARORRALKEEBEKEEBEKEEBEAGTIAIILDSGSDIDPDPORADFI 225
Qy 180 KDVMKLSNTSYQ--FAVOPSTSYKTEPDSYVKKRDPALAKHYGML--LTNTF 234
Db 226 SNNKRNTRYKKEFECNPLVQYGVITQTFBLRD--SODVWASLARQNTIQVGSVTKTA 282
Qy 235 GAINVYATEVERREELGARPATKYLLIITDG-----EATDSGNDAKDIIRYIIGIG 287
Db 283 SAMQHVLDSIFTSHGSRKRSKXVMVVLTDGIGFEDPLNITVINSPKMGQVEHFAIGVG 342
Qy 288 KHPQKESQETLHKFASKPASEFVKILDTFEKLDKLTTELQKTIYVLEGTSCODLTSPFM 347
Db 343 EEFKSARTARELNLIADPDETHAFKVTNWMALDGLSKLRVNIISMEGTVDGAL--HY 399
Qy 348 ELSSSGISAD-LSHGHAHVGAAGKDWAGGLDKALDODTFIGNEPITPEVRA-- 401
Db 400 QLAQIGFSAQILDERQVYLGAVGFWDMSGALLYDTSRKRGRF-NQTAADADAERAOX 458
Qy 402 GYLQYTWLPSRKQTSLLA--SGAPRYOHMGRAVLFQEPQGGGMSQVQTHGTQIGSY 459
Db 459 SYLVAAVAVL--HKTGSLSYVAGAPQYKHNAN--FELQKGEGBAFLPLVLEBQSGSY 513
Qy 460 FGGELGVVDVDDGETELLIGAPLFYGBORGGHVFYQ--RROLGEBEVSLEGGDPGYP 517
Db 514 FGSSELCPVDIDMDSTFLVLAAPFYVHGBEGGVYVYRLEBQDGSFSLARILLEGHGFT 573
Qy 518 LGRFGEALITLTDINGGLVDVAAGAPLEBEGA-----VYTFNRHGGSLSPQSORI 569
Db 574 NARFGPMAAMAGDLSQKLTIDVALGAPLBEGADGASFGSVIYNHMGDLSLSPSORI 633
Qy 570 EGTQVLSGIQWFGRSIHGVNLEGGDLADVAVAGASQMTVLSRPVVDVNTLMSFSPAL 629
Db 634 RASTVAPQLQYFGMSMAGGFDISGDGLADITVGLTGAVVFRRSPVVRKLYSMAFTSAL 693
Qy 630 PVHEVECSYSTSNKKEGVNITTCFOIKSLYPOQ-GRIVANLTYTTLQDLGHRTRRGLF 688

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Db 694 PI-----GENGVNVRNLCPEISSVTTASESGIREALLNFTLDDVDGKORR--- 739  
Qy 689 PGRHEHLEARNIAVTTSMCTD-----FSFHPVCVDLISPI 725  
Db 740 -----LQSDVRSGLGLARMSSGSGQLCEDLLMPTREGELCEBDCRSNA 783  
Qy 726 NVSLNLSLMEEGPTPRDRAQGXDIPTLL-RPSLSHSEWLEPFEXKNCEDKKCEANTRVS 784  
Db 784 SVKXSVYQQTDEG-----QTDHPQPLIDRYTEBPFAFQDLPYBACCNKRLFCVAELQLA 836  
Qy 785 FSPARSRLRLTAFAFASLVELSLNLEDAVWODLHFPPLGSLPRKXEMLKPSQIPVS 844  
Db 837 -TYSQQLVVLGVLTKELTLNINLTNSGSDSTMTSMALNYPNNLQKR--MOKPPSP-NIQ 892  
Qy 845 CEE-LPEESRLLSRALSCNVSSPIFK--AGSHVALQMFTNLYNWSGDSVELEHANYTC 900  
Db 893 CDDQPPVASFVLI---MNCRIQHPVLKRSASAVSVWQLEENAPPR---TADITVYTN 945  
Qy 901 MNBSDDLLEDSATT---ILPILYPINILLQODEDSLTVYS-----FTPKCP 944  
Db 946 SNERRSLANETHHTLQFRHGFVAVL-----SKPSIMYNTNQGSLSHKEPLFHVHGE 996  
Qy 945 KIHQVQKMYQVRIOPSIDHNHNPITLNAVGVPRPSEGRITNOMSVOMEPRVPCHYEDLE 1004  
Db 997 NLPGAEYLOQLCVPRKRLAGLOVAANKLT-----RTQASTVCTWSQER---ACATSSVQ 1047  
Qy 1005 RLPGAEPCLPGALFRCPVFRQET-----LVQVIGTLELVGEIEASMSPLSCSLSI 1057  
Db 1048 HVEEHVSVSCVIASDKENVVAAEISMDHSBELLDKVDTELQILGE-----I 1093  
Qy 1058 SFNSKRNHLX-GSNASLAQVMKVDVYBEKOMLY---LVVLSIGGLLMLLPIVLY 1112  
Db 1094 SFNNS---LYEGNAENHRT--KITVFLDKEXHSUPIIILKSGVGLVLIIVLIVLI 1147  
Qy 1113 KVGFPEKNLKE 1123  
Db 1148 KCGFFKRYQK 1158

RESULT 11  
S44142  
VLA-2 protein homolog - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C.Accession: S44142  
R.Edelman, J.M.; Chan, B.W.; Uniyal, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L.; Latze  
A.Description: The mouse VLA-2 homologue supports collagen and laminin adhesion but not  
A.Reference number: S44142  
A.Accession: S44142  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-1178 <DB>  
A.Cross-references: UNIPROT:Q62469; EMBL:Z29987; NID:G473098; PIDN:CA682877.1; PID:G4730  
F:169-344/Domain: von Willebrand factor type A repeat homology <WMA>

Query Match 15.7%; Score 959; DB 2; Length 1178;  
Best Local Similarity 27.5%; Pred. No. 1.2e-57;  
Matches 334; Conservative 219; Mismatches 468; Indels 194; Gaps 54;

Qy 25 SYNLDVGARBFSPPRGRHFGYRVLOV---GNGVIYGARPEG---NSGSLQOC--QS 75  
Db 26 AYVNGVGRPAKIFSGP-SEQRFYSVQDLTNQGMWLVGSPSGPFRKMDGVTKCPVDL 84  
Qy 76 GTGHCCLPVLKGSN-----YTSKYLGMTLATDPTVGSILACDGLSRTCDQNTYLSG 127  
Db 85 PTATCEKLNLDNSASISNVTEIKTNMSLGLTLTNPGTGFGLTGLPLMAHQCGQYVATG 144  
Qy 128 LCYIFRQNLQ-----GPMLOGRPGFQECIKCNVDLVFLFDGSMGLQDPEOK--ILDPMK 180  
Db 145 ICSVSVSPQGLTFSFPAVQACPSL-----VVVVVVCESNSIITYPEAVKNNLVFVVT 197

QY	181	--DWMKLSNTS	XOFAAQSTSVKTEPDSVDYKRD--	PDALLKHVMGMLLNTTPCAI	237
Db	198	GLDDEPKTK----	QVALLQYANBERIIIFNLNDFETKEKVMQATSETRHGGDLNTPRAI		253
QY	238	NYVATEVERREELGAR	PDATKVLIIITIGEATDSGNIDA-----	KDIIIRYIIGI-----	286
Db	254	EPARDYAQSOTSGGR	PGATKVMVVVVDDESHDGSKLTKVIOQCNDDIELRFGIAVLGYLN		313
QY	287	GKHQTKESQSTLKHFK	FAKPKASE--FVKILDPFELKXDLFTELQKKIYIIEGTSKODLTSF		345
Db	314	RNALDTKULKEIKAIN	ASTPTEHYFFFNVAADALALKRGT--LGEQIFISIEGT--VOGGDNF		371
QY	346	NMELSSGISADLSR	GHAHV--VGAIVGAKDMAGGFLELAD-----	LQDPTFIGNEPLTEPEV	399
Db	372	QMEMAQVFSADYAP	QNDIMLGNVAGFAWDSGLTQVETSHKPVIFPKAF--	DQVLODRN	429
QY	400	PAGYIGYVTWLP	PSRQKTSLLASGAPRYQHMGRVLLFOEPQGGHMSVOYITHGTQISY		459
Db	430	HSSFIGYSVAALIST	EDGVHFVA--GAPRANYTGOIILYSVNK--QGVVTVIOSHRCQOISY		487
QY	460	FGGELCGVDVQDDE	TELLIGALPFGCE--ORGRVITIGYRQIQPFEVBELQDDPYV		517
Db	488	FGSVLCSVDVQKDT	ITTDVLGALPTYMDLKKERKVLFTTTGILMQHOPLBEPBEGTG		547
QY	518	LGRFGEAITALT	DINGDGLVDVAVGAPLREO--GAVYIFNGRHGSLSPQSORIETGO--		573
Db	548	NARFOSAIALSD	INMOGFDNVIVGSPVENSGAVYIYNHQHGTIRKYSQKILGNSGA		607
QY	574	VLSGIQWGRSIRH	GVKOLEGDLADVAGASQMTVLSRKYVDVMTLMSRPAEIPVHE		633
Db	608	FRRLHGFGRSLD	GVGLNDGSIITDVSIGALGOVIQWMSOSIADVAIBALTPDXTITLLN		667
QY	634	VECSYSTNKKEG	EVNITICQIOLSLYPOFGARVAVNL--TYTLOLDGHTR--	BRGLP--P	689
Db	668	KDAK-----	ITLKLCPRAE--FRAGQNNQVAILFNMTLADGHSSVTSKGVRE		716
QY	690	GGRHELRRNIA	VTTSMSCTD--FSFHFPVCYQDILSPIVNSLNFSLMBEBSGTPRDQRAOG		747
Db	717	NSERFLQKQWVNE	VOKCSBHHIIOKP---SDVAVNPDLRLVDIST--ENPQT-----		764
QY	748	KDIPILRPSL--	HSET---WEIPFKNCGEEDKCEANLRYVSPASRSLRLTFA-----		798
Db	765	-----	SPALAYSEIYKVSIFPFYECGSDGICISDILLDQV--QLPALQOTOSFIYSN		815
QY	799	--ASLVELSL	ISNLEBDAVYVQDLHPBPGLSPFKVEMLKPHSOIYVSCBELPEBSRLLS		856
Db	816	QNKULTFSEVIL	KNGESAYNTVVLAEFSENLFPASFSM-----	PVDGTEVTCGVGSSQ	868
QY	857	RALSCNNVSP	FKXGHSYALOMENVTLVNSKGSVSELHANVTCNNESDLE--DNSKTT		915
Db	869	KSVTCDVGYPAL	KSEQVTFITINDFNLQNLQNOAA---INFOAPSESOETNKKADNSYL		925
QY	916	IIPILYIPINI-----	LFQODBSLTLYSFTPKGGRKIQVKMYQVRIQOPSIRD		963
Db	926	TIPILLYDAELH	LTSTNINFEISDENAPSVIISVEDIGKPF-----IFELKTYAG---		977
QY	964	HNIFLTLEAVV--	GVPQPPSE--GPITHQMSVOMER--PVPCHYE--DLERLPPAABCPLEGA		1017
Db	978	-SAEVSMALVTI	HPYTKENKPLLYLGLQTDQAGISCTAEINPLKLPHTA-----	PSV	1032
QY	1018	LFR-----	CPVV-----FRQELIYQVIGTLEIYGEIASMSWF---	S	105
Db	1033	SFKQENFRHYKEL	DCRTTSCSNITCMLKDLHMKAKBYFNV--	TRVWNRTPRAASFPQTVQ	1096
QY	1051	LCSSLSISFNS	SKRPHLYGSSNASTAOVVMKVADVUYEKOMLTYLVLG--	IGGLLILLILIF	1108
Db	1091	LTAABIDITHN	PQFLVIBENAVTIPLMIMKPT---EKAEVPTGVIIIGIINGILLILLAMT		1147
QY	1109	IVLYKVGFPK	NLKE	1123	
Db	1148	AGLWKLGF	FPKQYK	1162	



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RESULT 12
158409
Integrin alpha-9 chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 158409; A49459
R:Hihi, K.; Yamakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari, M.; Uchida, K.; Takah
Onogene 9, 611-619, 1994
A>Title: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in small
A:Reference number: 158409; MUID:94119603; PMID:8290272
A:Accession: 158409
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1035 <RES>
A:Cross-references: UNIPROT:Q13797; GB:D25303; NID:9464180; PDB:BA04984.1; PID:9533327
R:Palmer, E.L.; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D.
J. Cell Biol. 123, 1289-1297, 1993
A>Title: Sequence and tissue distribution of the integrin alpha9 subunit, a novel partne
A:Reference number: A49459; MUID:94064789; PMID:8245132
A:Accession: A49459
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 30-1035 <PAL>
A:Cross-references: GB:L24158
C:Superfamily: integrin alpha-4 chain
C:Keywords: glycoprotein; metal binding; transmembrane protein
F:1-27/Domain: signal sequence #status predicted <SIG>

Query Match 11.1%; Score 678.5; DB 2; Length 1035;
Best Local Similarity 23.1%; Pred. No. 2,5e-38;
Matches 289; Conservative 190; Mismatches 391; Indels 381; Gaps 53;

QY 22 PASYNLDVGARSFSPRAGHFGYRYLVQVNG-----VIVGAPGEGN-----STGSL 70
DB 26 PAGAVNLDPQRFVHFGP-ADSFQYAVLHFNHDTNRYLVGAPADSKYSPSVSPAV 84
QY 71 YQCGSGTG---HCLPVTL-RGSN-----YTSKYLGMTLATP-TDGSILADP 113
DB 85 FCRHTNPDRCTELDMARGNKRGTSCKGTCREDDEMMGVSLARPKADGVTACAH 144
QY 114 GLSRTCDONTYLS-----GLCYLFRONLQGMLOGR---PGFQECIKGNVDLVFLPDG 163
DB 145 RM-----KRIYEAHHLPHGFCYIIPSNLA---KGTLLPCYE----- 182
QY 164 SMSLOPDEFQKILDFMKDVMKKLSNTSYQFAVQPSYKTEFDFSDYVKRDPALLKH 223
DB 183 -----YKKKYG----- 188
QY 224 VAKMLLNTFGAIVYATEVFRBELGAPDPAKVLIIITDGEATDGNIDAKDIIRYI 283
DB 189 -----EEHGS----- 193
QY 284 IGIGHFQTKESQETLHKFASKPASEFKLIDTFEKLKDLFTLEOKKIVIBGTSKOLY 343
DB 194 ----- 193
QY 344 SFNMELSSSGISADLSRGHAAVAVGAWAGGFLDLKADLODDTFIG-NEPLTEPVAG 402
DB 194 -----CQAGIAGFTBELVWVGAGSFWAGTIKVL-NLTDNYLKLNDDEVINNRYYT 245
QY 403 YLGIYVT-WLPSRQKTSLSLAGAPRYQIMGRVLLFOEPQGGHWSOVOTIHGTQIGSYFG 461
DB 246 YLGIYVTAGHFSHPSTIDVVGAPQDKIGIKYIIFRARRSGTLLKIFQASGKKMGSYFG 305
QY 462 GELGVVDVDOGETELLIGAPLFGEGQGRGVFIYQROG-FREVELEGDPPEYRGR 520
DB 306 SSLCAVDLNGDELSD-LVAGAPMSSIRDEGOVTVYINRGKALBEQLALTGDGAYN-AH 363
QY 521 FGEATLTALDINGDGLVDAVGAPELEQ--GAVYIFNGHGGISLPQSORIEGTQVLSGI 578
DB 364 FGEASIASLDDLNDGFPDVAIGAPKEDDPAGAVVIYHGDAGGIVPQYMKLSGQKINVL 423
QY 579 QMFGSHIGVDLBDGDLADVAVGA--ESQMIVLSRPVDMVTMLMSFPAEIPVHAEVC 636

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DB 424 RMFGQISISGIDMDNGENPVTVGAFMSDSVLLRARFVI-TVVDSIFLPESITITPQC 482
QY 637 SYSTSNKREKQVNTITFCFQIKSLVPQGRVY---ANLYTTLQIDGHTRRRLGP---- 689
DB 483 --HDGQPPVNCIANTVTCF-----SFHGKVPBEIEGLANYLMDVAK-KEQGMPIRVF 532
QY 690 ----GGHELRNIAVY-TSMSCDPSFHPVPCYQDILSPINVSLSMEBETPPDQR 744
DB 533 VLIGETVQVTEKQLQITMEERTCHYVAHVRRQDVISPVEBAAST-SEHYTGEER 591
QY 745 AQGDIPPIILPSSL-----SETWEIPEKN-----CGEDKCEANLRFSPARSRA 792
DB 592 ----ELPP-LTPVLRMKKGQKIQAQKQTVFERKRSRSDCAADLOQKLLISNDEKTYL 646
QY 793 LRLTAFASLSVELSLNLEBDAYVVDLHFPPLSF---RKYEMLKPSHQPVSCEEL 848
DB 647 LALGAVKNISINISINLGDADYDANVSFNVSRLEFLTNMWOKEEM-----DISCELL 699
QY 849 PEESRLSLRSLSCVSSPIFRAGSHVALQMMFNTLVNSMGDSVELHANYTC--NNEDS 905
DB 700 E-----SDFLKCSGVGFPMRSKSKYEFVYFDTSHLS--GEERVLSPITYAOGSNTERS 751
QY 906 DLLEDNSATITPLIYPINILIQDQEDSTLYVSTPRGPKIHQY-----HMQVR 956
DB 752 ESLHDNTLVLMPLMHEVDVSTIGMSPTSFV---YGESVDANFTQLDDLECHFPQIN 807
QY 957 IQPSIHD---HNITPLEAVGVPPQPSGPTTHQMSVQ-----MEPPVPC-- 998
DB 808 ITLQVNTGPTLPGSSVSISFPRRLSSG-ALMFHYQEMVVGQKNGCRQKPTFCII 866
QY 999 --HYEDI-----ERLPDAEPCLPGLFRC-DVFERQ--ILVOVIGTLEL 1039
DB 867 PQEQENFHTIFAFFTSGKRVLDCEKRGISCLTAHCNPSALAKESRTIDYMLNTEI 926
QY 1040 VGETEASMSLSGSLISIRNS-KHFLYGSNLSLAQVMKVUVYK-----QM 1089
DB 927 LKK-DSSSVIQFMRARVAKDPAALVVEIAHGNE-----EVVVEALHNTEPRGYV 979
QY 1090 LYLVLVSGIGGLLLLLIFLYLVKGFENLKEKMEAGRVPGIAPDS 1140
DB 980 GMITAIELVGIILFLLAVLVMCMGFFRRRYKIIIEAK--NRKENEDS 1027

RESULT 13
A1131
Lymphocyte-Peyer's patch adhesion molecule alpha 4 precursor - mouse
N:Alternate names: Integrin alpha-4
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41131; S16742
R:Neuhaus, H.; Hu, M.C.T.; Hemler, M.E.; Takada, Y.; Holzman, B.; Weissman, I.L.
J. Cell Biol. 115, 1149-1158, 1991
A>Title: Cloning and expression of cDNAs for the alpha subunit of the murine lymphocyte-1
A:Reference number: A41131; MUID:92064645; PMID:1840602
A:Accession: A41131
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1039 <NEU>
A:Cross-references: UNIPROT:Q00651; EMBL:X53176; NID:951484; PDB:CAA37316.1; PID:951485
C:Superfamily: integrin alpha-4 chain
C:Keywords: cytoskeleton; transmembrane protein

Query Match 10.4%; Score 633; DB 2; Length 1039;
Best Local Similarity 23.4%; Pred. No. 3,6e-35;
Matches 285; Conservative 193; Mismatches 425; Indels 316; Gaps 54;

QY 6 ITVAMALLSGFFFPASSYNLDVGARSFSPRAGHFGYRYLVQVNG-----VIVGAP 61
DB 21 IALREAVMLLYFGVPGPSYNLDPENALLYQGP-SGTLFGYSVVLHSHSGSKRLIYGAP 79
QY 62 GEGNSTGSLVQCGSGTGHCLPVTLRGSNTSKYLGMLTADPDGSLIACDPG-----SR 117

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Db 80 -----TASWLSNANVNP--GAIYRC--GIKRNENQ 106
Qy 118 TCDONTYLSGLCYLFRONLQGPMLQGRPGFOECIKANVDVLFDFGSMLSLPDEROKLTD 177
Db 107 TCBO-----LQSGSPGEGPCGKTCLEER-DNQWL-GVITLSRQGERGSI-- 148
Qy 178 FMKQVMKLSNTSYQFAAVQPSSTYKTEPFDSYVK--RKPDALLKRVKMLLTNTFG 235
Db 149 -----VTCGRHWKNIF-----VYKSDNKLPT----- 169
Qy 236 AINVAATEVPREELGARDATKVLIIITDGEATDSGNIDAKDIIIRYIIGIKHFQYKES 295
Db 170 GICVYMPEDLRTLSKR-----MAPCYKDYLR----- 196
Qy 296 QETLHKFASPKASEPVKILDTFEKLKDLFTELKIKYIIEGTSKQDLTSFMNMLSSSGIS 355
Db 197 -----KREBNPAS-----CQAGIS 210
Qy 356 ADLSRGHAVVAGVAKDMAGG-FLDLKADLDDPTIGNEPLTPPEVRAG-VLGYTVTWLPS 413
Db 211 SFYTODLIVMGAPGSSYWTGTVFVYNTTNQYKAFVDRQ---NQYKFGSYLGYVAGAHF 267
Qy 414 RQ-KTSLASGAPRYQHMGRVLLPOEPGCGGMSQVOTIHGTQIGSYFGELGVDVDQD 472
Db 268 RSPHTEVVGAPQHBOIGKAYISIDE--NELNIVYEMKKGKUGSYGASVCAVDLAD 325
Qy 473 GETELLIGADLFYGEORGRGVFIYORQLG---FEVSELSQDGPYGLGRFEALTYLT 529
Db 326 GFSD-LIVGAPMOSITREGRVFIYINGMGANVMEMRVLVGSKY-AAAFGESIANLG 383
Qy 530 DINGEDLVAVAPLEB--QGAVYIFNGRHGGLSPQSORIETGTVLSGIQWFGRSIHG 587
Db 384 DIDMGFEFDIAIGAPQBDLRGAVYIYNGRVDSISSTYQRIEGQIISKLRMGQGISG 443
Qy 588 VKDLBGDLADVAIGA--ESQMIYLSRPVVDMTLMSFSPAELPVHEVBCSYSTSNMK 645
Db 444 QIDDMNNGYVVAAGAFQSDSAVLLRTRPVYIVASLS-HBESVNRKTFDC---TENGLP 499
Qy 646 E-GVNTITFOIKSLYPOFQGRVLANLYTTLQDLQHR---TRBRGLPGGRHE-LRNLI 699
Db 500 SVCHNLITLCSYK--KEVPGYIV-LFTVNSLDVHRABSPRSRYFSSNOSTVITGSI 555
Qy 700 AVTTS-MSTDPFSHPVQVDLISPIVNSLNFSLMEEGTPRDQAGKDIPIPLRPSL 758
Db 556 RVSSSGEKCTHQAFMRKQVDILTRPIHEATYHLGHVITKRN---EEFPP-LQDIL 610
Qy 759 HSEFW-----IPEKNGCEDKCCENLRYS-----FSPARSA-LRLTLPASLSVELS 806
Db 611 QOKKEKQIVRMINFARPCAYE-NCSADLVSAKVGLPKPYENKTYLAVGSMKTIAMVS 669
Qy 807 LSNLEBDAYVQDLHPFPGLSFRKVBMLKPHSOIPVSCCELPPESRLLSRLASCONSP 866
Db 670 LPMAGDDVYETTLNVQLFTGLYFIKIDLE---EKQINC-EVYSSGVYK--LACSGLYI 723
Qy 867 IFKAGHSVALQOMENTLVNSWGDSEVELHANVTGNNE--DSDLLEBNSATITIIPIIYPINI 925
Db 724 YVDRLSRIDISFLDVSLSRAHEDLSISVHASCENBELDQVADNRTLTILPIRYEML 783
Qy 926 LIQOQBSTLYV-----SFTKPKRIHOVKMYOVRIPQSIHDHNIPTLBAVGVQ 977
Db 784 TVHGLVNTFSYVYSSSENEBETCAEBKDLNLFVYINTGISMA-----PWSYKIMWPN 837
Qy 978 P--PSEGITHOMSVQMPRPVPCYEDLERLPDAABPCLPGALFRCPVPVFOELIVQIG 1035
Db 838 SFLFQDDGLFVNLVDQTTG-QCHFKAQR-----ECTFAQCKGIAGLTLD 882
Qy 1036 TLELVGELIASSMSL-----CSSLSISF-----NSSKPFHYG-----SNASIAQ 1076
Db 883 IVKFLSKTDKRLYCMKADQHCPLCNFGMSGSKASVHIQLEGRSIEMEMETSIX 942
Qy 1077 VVMK-----VDVYVEKQMLYV-----LSGIGLALLILI 1107
Db 943 FEIKATAPPEBHPKVIILNKDENVAHVLBGLHHQRPGRHFTIIITISLIGLIVLLI 1002
```

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Qy 1108 FIVLYKVPFKRNLIKEMK 1126
Db 1003 SCVMMKAGFFKRYOKSLIQ 1021

RESULT 14
506046
Integrin alpha-4 chain precursor - human
N:Alternate names: CD49d; very late antigen-4 alpha chain; VLA-4 alpha chain
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence, revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: 506046; A39355; D28018
R:Takada, Y.; Ellices, M.J.; Crouse, C.; Hemler, M.E.
EMBO J. 8, 1361-1368, 1989
A:Title: The primary structure of the alpha(4) subunit of VLA-4: homology to other integr
A:Reference number: 506046; MUID:89356603; PMID:2788572
A:Accession: 506046
A:Molecule type: mRNA
A:Residues: 1-1038 <TAK>
A:Cross-references: UNIPROT:P13612; GB:X16983; EMBL:X15356; NID:g33945; PIDD:CAA34852.1;
R:Rosen, G.D.; Birkenmeier, T.M.; Dean, D.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 4094-4098, 1991
A:Title: Characterization of the alpha-4 integrin gene promoter.
A:Reference number: A39355; MUID:91239513; PMID:2034655
A:Accession: A39355
A:Molecule type: DNA
A:Residues: 1-93 <ROS>
A:Cross-references: GB:M62841
R:Takada, Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A:Title: The very late antigen family of heterodimers is part of a superfamily of molecu
A:Reference number: A94151; MUID:87204112; PMID:3033641
A:Accession: D28018
A:Molecule type: Protein
A:Residues: 40-50; 'E', 52-53 <TA2>
A:Genetics:
A:Gene: GDB:ITGA4; CD49D
A:Cross-references: GDB:128032; OMIM:192975
A:Map position: 2q31-2q32
C:Superfamily: Integrin alpha-4 chain
C:Keywords: cell adhesion; cytoskeleton; duplication; glycoprotein; heterodimer; transmem
F:1-39/Domin: signal sequence #status predicted <SIG>
F:40-1038/Product: integrin VLA-4 alpha-4 chain #status predicted <MAT>

Query Match 10.1%; Score 619.5; DB 2; Length 1038;
Best local similarity 25.9%; Pred. No. 3.1e-34;
Matches 235; Conservative 168; Mismatches 337; Indels 169; Gaps 44;

Qy 322 DLFTLEOKKIYVIEGTSKOD-LTSFMNELSS--SGISADLSRGHAVVAGVAKDMAGGFL 378
Db 177 DLRTLSKRI-----APCYQDYVKKFGENFASCOAGISSFTTKOLIWMGAPGSSYWTGSLF 232
Qy 379 -----DLKA--DLDDPTIGNEPLTPPEVRAGYLVYTWLPSR-QKTSILASGAPRYQ 428
Db 233 VYNIITTKYKAPLDKQVQVFGS-----YLGSVGAHGFRRGHTTEVVGAPQHE 282
Qy 429 HMGRLVLLFQEPQGGGHSQVQTH---GTQIGSYFGELGCVVDQDGETELLIGAPL 485
Db 283 QIGKAYIFSIDE-----KELNIILHEMKKGKLGSYFASVCAVDLADGFSQD-LLVGAPMQ 336
Qy 486 YGSGRGRVFIYORQLG---EVSSELQDGPYGLGRFEALTYLTIDINGDLVAVAG 542
Db 337 STIREGRVFIYINGSGAVMMNMTNLVGSQYK-AAAFGESIYNLGDINDGFEVDYATG 395
Qy 543 APLEB--QGAVYIFNGRHGGLSPQSORIETGTVLSGIQWFGRSIHGVQDLBEGDLADVA 600
Db 396 APQEDDLQGAIVLYNGBADGISSTFSQRIEGLDISLSMFGGSIQGDADANNQGYDVA 455
Qy 601 VGA--ESQMIYLSRPVVDMTLMSFSPAELPVHEVBCSYSTSNKKEG-----VNTITC 653
Db 456 VGARFSDSAVLLRTRPVYIVDAISL-HBESVNRKTFDC-----VENGPVSCIDILYIC 507
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QY 654 FOIKSLYPOFOGRVLAANTLYTTLQDGHRTTR--RGLFP--GGRHELRNIAVTT--SMSC 707  
DB 508 FSYKQ--KEVGYIY--LFTNMSLDVNRKAKSPFPFYSSNCTSVITGSIQVSSREANC 563  
QY 708 TDFSHFPVVCODLISPINVSINFSLMEBEGTPRDORAQKDIPIRLPSLHSETWE--- 764  
DB 564 RTHQAFMRKQVDILTIPIQIEAAHYL-----GPHVLSKSTEEFP--LQPILOQKKEKIDIM 618  
QY 765 ---IIFEKQCGEDKCEANLRYS-----FSPARSA-LRLTAFASLSVELSLNEEDAY 815  
DB 619 KKTINFARFCAHE--NCSADLQVSAKIGFLKPHENKTYLAVGSMTKLMLNVSILFNAGDAY 677  
QY 816 WQULHHPGGLSFKRVEMLKPHSQIPVSCBELPESBLLSALUSCONSSPIFFKAGSVA 875  
DB 678 ETTLHVAKLPVGLYFKILIELE---EKQINC--EVTNMSGVQ--LDCSIG--YIYVDLSR 729  
QY 876 LQMMF---NTLVNSWGDVVELAHANVTCONNEDS--DLLEDNSATTIIPILYINILIOD- 929  
DB 730 IDISFLDVSSLSRABEDLSITVHA--TCENEBENDLKHSHVYVAIPLKTEVKLTIVAGF 787  
QY 930 -QBDSTLYVSTTPKPKTHQVKMYQVRIQPSIHDHNIPTLEAVVGVQ--PPSEGPITH 986  
DB 788 VNPFSFVYSGSDNENPEFCWVEKMLTFHVINTGSMAPNVSVIEIMVENSFSQTDKLFN 847  
QY 987 QMSVQMEPPVPCHYEDLERLPDAAPCLBGLFRCPVVFROEILVOVIGTLEVGEITAS 1046  
DB 848 ILDVOTTTG--ECHFENYQV-----CALBOQKSNMOTLKGIVAFLSKTDKR 892  
QY 1047 SMFSL-----CSSLSISF-----NSSKHFLYQ----- 1069  
DB 893 LLYICKADPHCLNFCNGKSHESGEASVHTQLEBRPSILEMDETSALKFEIRATGPPEP 952  
QY 1070 -----SNASLAOVNKKDVVYEKQMLYLYVL-----SGIGGLLLLLLIFIVLYKGVFP 1117  
DB 953 NPRVIELKNDENVAVHLE--GLHQRPKRYFTIIVISSLLGLIVLLISVVMKAGFF 1011  
QY 1118 KRNLEKME 1126  
DB 1012 KRQYSLIQ 1020

## RESULT 15

Integrin alpha chain SU2 - sea urchin (Lytechinus variegatus)

C.Species: Lytechinus variegatus (variegated urchin)

C.Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C.Accession: T31437

R:Hertzler, P.L.; McGilay, D.R.

submitted to the EMBL Data Library, May 1998

A.Description: Alpha SU2, a sea urchin integrin which binds laminin.

A.Reference number: Z21035

A.Accession: T31437

A.Structure: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-1041 <HER>

A.Cross-references: UNIPROT:O76378; EMBL:AF067658; NID:G3220240; PID:G3220241; PIDN:AAC2

A.Experimental source: developmental stage embryo

A.Function:

A.Description: binds laminin

C:Superfamily: integrin alpha-2b chain

Query Match 9.6%; Score 588; DB 2; Length 1041;

Best Local Similarity 22.5%; Pred. No. 4.7e-32;

Matches 289; Conservative 199; Mismatches 407; Indels 392; Gaps 61;

QY 9 MAMALLSGFF---FAPASSVNLVDRGARSFSPRAGHGGYRVLOVNG---YVIGAP 61  
DB 1 MARILLISFYAILLDSTAGFNFDLAPLKFDPG--DGSNFGSVQHRDGTMDALVGAP 59  
QY 62 -----GEGNSTGSLVQCOSGTGHC--LPTVLGRS---NYSKYIAGMTLATDPMDG 106  
DB 60 EASTNOSGVTGKGAIVYSVCRLSPSVCEQIIPFDKGTGINNVNDKSNQMFQATVVASGANG 119

QY 107 SIACDPGLSRTCDQNTYLSGLCYLFRONLQGPMLQGRPGHQEICKGNVDLVPFLPDSMS 166  
DB 120 QILKCAPRL-----VWVETASVTKROEHEPFGTQFVGSD---FTMFVN 160  
QY 167 LQDPFQKILDPMKDVNKKLSNNTSYOPAAVOFSTSYKTEPFDSDYVKKRDPALLKHYKH 226  
DB 161 YSPQSTNRELYGD---KITHQAGFSGLIFS-----DMSALV----- 196  
QY 227 MLLTLTTFGAINVYATEVFREBELCARPDATKVLIIITDGEATDSGNIDAKDITRIYIGI 286  
DB 197 -----MGA----- 199  
QY 287 GKHPQTESQETLHKFASKPASEPVKILDPFEKLDLFTLEOKTY-----VIBGTS 338  
DB 200 -----PESYV-----LQGIYVQSLNRSVQATQ 224  
QY 339 KQDLTSFNMELSSSGISADLSRGAHVAGAKMAGGFLDKKADLDDPFIQNEPLRPE 398  
DB 225 ESNVTGTSFDSYNGYSLALG-----DFND----- 250  
QY 399 VRAGYLGTYVTWLPBSROKTSILASGAPRYOH--MGRVLLPOEPQGGGHWVQVTHGTQIG 457  
DB 251 ---GVQDYVV-----GTPRASELMGLVAFIDQ---NLNQFNQVWGTQIV 288  
QY 458 SYRGEELQGVVDQDGETELLIGAPLYGB-----QR--GGRVPIY--QRQLG-----F 504  
DB 289 AYPFYSVTVVDINDTYDD--LVGAPYMDGPALQRMGAAYVYVQLNPDVGRASNL 347  
QY 505 EEVVELQDDPGYPLGRFGEATITALTIDNGDLVAVAGAPLE--EOGAVYFNGRHGLS 562  
DB 348 SLSTSLIG--QGISRRTGLSIASIGDSNQGFNDVAVIGAPFEGSDAGAVYIYHSANGLK 405  
QY 563 POPSQRI--EGTQVLSGIQWFGRSIHGVKDLGEGDLADVAGAES--QMTVLSRPVYDMV 619  
DB 406 STPAQVLTPLSTLHSGGITTFFGFSLQGGQMDKXKYPDLVGAESANVAVILRTRPVVSLD 465  
QY 620 TLMSPSPAEIPVHVEBSYSTSNMKEGVNIT-----ICPQIKSLY--POPGRLVANLTY 673  
DB 466 ATLNTPEPLGINLE-----NKTVELADGTWTSPIAMTCFTYTGNYLBDH-----IDISY 514  
QY 674 TLQD--GHRTRRGLF--PGGRHEL--RRNIAVTTSMSCDPSFHFPCVODLISPINVS 729  
DB 515 TVTVDSGIANRRAMFMDNDMSBITTKRRLAVSTQF--CDPLRAYVGSIEBKLTPIKVTL 573  
QY 730 NFSLMEBEGTPRDORAQKDIPIPL--RPSLSHSETWEIPEKNCGEKCKCEANLVSFSPA 788  
DB 574 QYDLNND-----SRLOPHETLPIIDMATKSTQKQVSIQNC--VNNICIPDLDTVTJPN 627  
QY 789 RSRALRLTAFASLSVELSLSLBEDAYWQDLHPFGSLFRKRYEMLKPHSQIPVSCBEL 848  
DB 628 LPNIV-IGQTOELTLVDVSLNNRGEAFQSSLSVYPPGLQFVRLER--KANNDPSVTS-- 683  
QY 849 PERSRLSRALSNVSCVSPIFRAGHSV--ALQMMFPTLVNSMSGDVELAHANVTC--NNESD 906  
DB 684 -EDSDL--RIITCTGNPM--VGKNILFEGTLTSFQVSGDKDSEIERYFKASENSBDPN 738  
QY 907 LLEBNSATVTLIPII-----VPINILIQDESDTVLVSTPKPKPIH----- 947  
DB 739 TLENNELMNTVYPVVDCTIKLKSASYPEIYWSQED---YV--VPPPPAAGAEADIGM 793  
QY 948 QVKEMYQVRIQPSIHDHNIPTLEAVVGPQPPSEGP--ITHQMSVQMEPPVPCHYEDLERL 1006  
DB 794 EVMHLYEVR---NTGSSNAGVSLINIQMPQKNEDGEVLYFYLLGIMTEBGVYCOLTOGKAN 850  
QY 1007 PDAA--EPC-----LPGALFRCPPVVFROEILVOVIGTLEVGEITASMFSLCS 1053  
DB 851 PEGYKLEPSTAKLSNNTQVSGKRKRPEV--AEALAQIDNVYTCASD---SCVLIINCT 905  
QY 1054 SLGISFNSKGFHLGY-----SNASIAQVVMKVDV----- 1083  
DB 906 IDEINASKSKVYRILGFWERTFOKAVSELTPVQVQATIASASAAVKTIPYNIPLPDPFS 965  
QY 1084 -----VYEKQML-----YLYVLSGIGILLLLLIIFIVLYKXGFFPRNLEKEMEA 1127

Db	966	DSTKASTLVTTBELVPPVTPIAMWIIYVSVLGGIILLLIILGLMKCGFPERKK-----	1019
Oy	1128	GRGVNNGIPAPDSE--OLASGOBAGDP	1152
Db	1020	-----PGEKEKAYAPVASADKDCGP	1038

Search completed: August 29, 2005, 19:24:24  
 Job time : 37 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 29, 2005, 19:12:58 ; Search time 114 Seconds  
(without alignment)

5255.550 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106

Sequence: 1 MKDSCITMANALLSGFFPP.....DPGLKPLHKDSGSGGKD 1170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	6106	100.0	1170	1	ITRL_HUMAN	P20701 homo sapien
2	5585	91.5	1086	2	Q96HBI	Q96HBI1 homo sapien
3	4657.5	76.3	1165	1	ITRL_BOVIN	P61625 bos taurus
4	4571.5	74.9	1166	2	Q6TYB8	Q6TYB8 bos taurus
5	4365.5	71.5	1161	2	Q9WTV4	Q9WTV4 mus musculus
6	4361	71.4	1160	2	Q9R200	Q9R200 mus musculus
7	4343.5	71.1	1163	1	ITRL_MOUSE	P24063 mus musculus
8	3644.5	59.7	927	2	Q8H2V0	Q8H2V0 bos taurus
9	1583.5	25.9	1188	2	Q6KRS4	Q6KRS4 mus musculus
10	1582.5	25.9	1169	1	ITRX_MOUSE	Q9QXB4 mus musculus
11	1562.5	25.6	1152	1	ITRX_HUMAN	P12115 homo sapien
12	1526.5	25.0	1163	1	ITRX_HUMAN	P20702 homo sapien
13	1516	24.8	1161	1	ITRX_RAT	Q9QYE7 ratu
14	1514.5	24.8	1153	1	ITRM_MOUSE	P05555 mus musculus
15	1488.5	24.4	1151	2	Q9J130	Q9J130 ratu
16	1476	24.2	1162	1	ITRD_HUMAN	Q13340 ratu
17	1442.5	23.6	1187	2	Q98TF0	Q98TF0 cyprin
18	1436.5	23.5	1196	2	Q98TF1	Q98TF1 cyprin
19	1243	20.4	920	2	Q28984	Q28984 sus scrofa
20	1154	18.9	1189	1	ITRH_HUMAN	Q9UKX5 homo sapien
21	1121	18.4	1188	1	ITRH_MOUSE	P61622 mus musculus
22	1118	18.3	1188	2	Q7TQC3	Q7TQC3 mus musculus
23	1114.5	18.3	1151	1	ITAI_HUMAN	P56199 homo sapien
24	1112.5	18.2	1180	1	ITAI_RAT	P18614 ratu
25	11105	18.1	1167	1	ITRG_HUMAN	P18578 homo sapien
26	1070.5	17.5	269	2	Q80WE9	Q80WE9 ratu
27	1012.5	16.6	1170	1	ITR2_BOVIN	P53710 bos taurus
28	1007.5	16.5	1167	2	Q88341	Q88341 ratu
29	995	16.3	1167	2	Q88340	Q88340 ratu
30	994	16.3	1171	2	Q42094	Q42094 galu
31	993	16.3	1167	1	ITR4_MOUSE	Q60677 mus musculus

32	985	16.1	1181	1	ITR2_HUMAN	P17301 homo sapien
33	976.5	16.0	1179	1	ITR4_MOUSE	P38570 homo sapien
34	959	15.7	1178	1	ITR2_MOUSE	Q62469 mus musculus
35	959	15.7	1178	2	Q6PIC7	Q6PIC7 mus musculus
36	907.5	14.9	1038	2	Q8BS01	Q8BS01 mus musculus
37	894.5	14.6	895	2	Q8WSP8	Q8WSP8 mus gp. itg
38	872	14.3	1160	2	Q8MKR4	Q8MKR4 felis silve
39	803	13.2	823	2	Q8WY18	Q8WY18 homo sapien
40	765.5	12.5	823	2	Q8CE84	Q8CE84 mus musculus
41	754.5	12.4	1332	2	Q8BPQ8	Q8BPQ8 halocynthia
42	679	11.1	1036	2	Q91YD5	Q91YD5 mus musculus
43	678.5	11.1	1035	1	ITR9_HUMAN	Q13797 homo sapien
44	668.5	10.9	780	2	Q06271	Q06271 xenopus lae
45	633	10.4	1039	1	ITR4_MOUSE	Q00651 mus musculus

#### ALIGNMENTS

RESULT 1  
ITRL\_HUMAN STANDARD; PRT; 1170 AA.  
ID P20701; Q43746; Q9UBC8;  
AC 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1  
DE alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha  
DE chain) (CD11a).  
CN Name=ITRGA; Synonyms=CD11A;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.  
RX MEDLINE=89139587; PubMed=2537322; DOI=10.1083/jcb.108.2.703;  
RA Larson R.S., Corbi A.L., Berman L., Springer T.;  
RT "Primary structure of the leukocyte function-associated molecule-1  
RT alpha subunit: an integrin with an embedded domain defining a protein  
RT superfamily";  
RL J. Cell Biol. 108:703-712(1989).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;  
RA Lofthus B.J., Kim U.-J., Sneddon V.P., Kalish F., Brandon R.,  
RA Puhmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,  
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,  
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;  
RT "Genome duplications and other features in 12 Mb of DNA sequence from  
RT human chromosome 16p and 16q.";  
RL Genomics 60:295-308(1999).  
RN [3]  
RP SEQUENCE OF 1-20 FROM N.A.  
RX MEDLINE=93281759; PubMed=8099450;  
RA Shelley C.S., Farokhzad O.C., Arnaout M.A.;  
RT "Identification of cell-specific and developmentally regulated nuclear  
RT factors that direct myeloid and lymphoid expression of the CD11a  
RT gene";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:5364-5368(1993).  
RN [4]  
RP SEQUENCE OF 1-20 FROM N.A.  
RX MEDLINE=93374910; PubMed=8103515;  
RA Nueda A., Lopez-Cabrera M., Vara A., Corbi A.L.;  
RT "Characterization of the CD11a (alpha L, LFA-1 alpha) integrin gene  
RT promoter.";  
RL J. Biol. Chem. 268:19305-19311(1993).  
RN [5]  
RP SEQUENCE OF 1-20 FROM N.A.  
RX PubMed=8097887;  
RA Cornwell R.D., Gollan K.A., Hickstein D.D.;  
RT "Description of the leukocyte function-associated antigen 1 (LFA-1 or  
RT CD11a) promoter.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 90:4221-4225(1993).
RN [6]
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 153-335, AND REVISION TO 214.
RX MEDLINE=96036067; PubMed=7479767;
RA Qu A., Leahy D.J.;
RT "Crystall structure of the I-domain from the CD11a/CD18 (LFA-1, alpha L
RT beta 2) integrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10277-10281(1995).
RN [7]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 153-335.
RX MEDLINE=96396882; PubMed=8805579; DOI=10.1016/S0969-2126(96)00100-1,
RA Qu A., Leahy D.J.;
RT "The role of the divalent cation in the structure of the I domain from
RT the CD11a/CD18 integrin.";
RL Structure 4:931-942(1996).
RN [8]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 153-334.
RX MEDLINE=99425288; PubMed=10493852; DOI=10.1006/jmbi.1999.3047;
RA Kallen J., Weizsaeck K., Rammge P., Geyl D., Kriwacki R., Legge G.,
RA Cotten S., Weitz-Schmidt G., Hommel U.;
RT "Structural basis for LFA-1 inhibition upon Iovastatin binding to the
RT CD11a I-domain.";
RL J. Mol. Biol. 292:1-9(1999).
CC -I- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM3, ICAM2,
CC ICAM3 and ICAM4. It is involved in a variety of immune phenomena
CC including leukocyte-endothelial cell interaction, cytotoxic T-cell
CC mediated killing, and antibody dependent killing by granulocytes
CC and monocytes.
CC -I- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
CC associates with beta-2.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P20701-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P20701-2; Sequence=VSP_002738;
CC Note=No experimental confirmation available;
CC -I- TISSUE SPECIFICITY: Leukocytes.
CC -I- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -I- SIMILARITY: Belongs to the integrin alpha chain family.
CC -I- SIMILARITY: Contains 7 FG-GAP repeats.
CC -I- SIMILARITY: Contains 1 VWFA domain.
CC -I- SIMILARITY: Contains 1 VWFA domain.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11a.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00796; CAA68747.1; -.
DR EMBL; AAC002310; AAC31672.1; -.
DR EMBL; M95609; AAA16474.2; -.
DR EMBL; Z22804; CAA80461.1; -.
DR EMBL; M87662; -; NOT ANNOTATED_CDS.
DR PIR; S03308; S03308.
DR PDB; 1COP; X-ray; A/B=153-334.
DR PDB; 1DGO; NMR; A=149-336.
DR PDB; 1LFA; X-ray; A/B=-.
DR PDB; 1MUN; X-ray; A=153-331.
DR PDB; 1MQ8; X-ray; B/D=155-331.
DR PDB; 1MOA; X-ray; A=152-330.
DR PDB; 1MOA; X-ray; A=152-330.
DR PDB; 1ZON; X-ray; @=150-336.
DR PDB; 1ZOO; X-ray; A/B=150-336.
DR PDB; 1ZOP; X-ray; A/B=150-336.
DR Genew; HGNC:6148; ITGAL.
DR MIM; 153370; -.

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DR	GO:	GO:0008305; C:integrin complex; TAs.
DR	GO:	GO:006928; P:cell motility; TAs.
DR	InterPro:	IPR000413; Integrin_alpha.
DR	InterPro:	IPR002035; VWF_A.
DR	Pfam:	PF01839; FG-GAP 3.
DR	Pfam:	PF00357; Integrin_alpha; 1.
DR	Pfam:	PF00092; VWA; 1.
DR	PRINTS:	PRO1185; INTEGRINA.
DR	PRINTS:	PRO0453; VWFADOMAIN.
DR	SMART:	SMO0191; Int_alpha; 5.
DR	SMART:	SMO0327; VWA; 1.
DR	PROSITE:	PSS00242; INTEGRIN_ALPHA; 1.
DR	PROSITE:	PSS0234; VWA; 1.
KW	3D-structure:	Alternative splicing; Calcium; Cell adhesion;
KW	Direct protein sequencing:	Glycoprotein; Integrin; Magnesium;
KW	Receptor; Repeat; Signal; Transmembrane.	
FT	SIGNAL	1 25
FT	CHAIN	26 1170
FT	DOMAIN	26 1090
FT	TRANSMEM	1091 1111
FT	DOMAIN	1112 1170
FT	REPEAT	42 91
FT	REPEAT	92 149
FT	DOMAIN	156 327
FT	REPEAT	350 400
FT	REPEAT	401 455
FT	REPEAT	457 516
FT	REPEAT	518 575
FT	REPEAT	578 630
FT	CA_BIND	468 476
FT	CA_BIND	530 538
FT	CA_BIND	590 598
FT	SITE	1115 1119
FT	DISULFID	73 80
FT	DISULFID	111 129
FT	DISULFID	653 707
FT	DISULFID	771 777
FT	DISULFID	845 861
FT	DISULFID	998 1013
FT	DISULFID	1021 1052
FT	CARBOHYD	65 65
FT	CARBOHYD	85 89
FT	CARBOHYD	188 188
FT	CARBOHYD	649 649
FT	CARBOHYD	670 670
FT	CARBOHYD	726 726
FT	CARBOHYD	730 730
FT	CARBOHYD	862 862
FT	CARBOHYD	885 885
FT	CARBOHYD	897 897
FT	CARBOHYD	1060 1060
FT	CARBOHYD	1071 1071
FT	VARSPLIC	954 954
FT	CONFLICT	214 214
FT	CONFLICT	660 660
FT	STRAND	155 162
FT	STRAND	164 164
FT	TURN	165 166
FT	HELIX	169 185
FT	TURN	186 188
FT	STRAND	191 198
FT	STRAND	202 206
FT	HELIX	208 214
FT	HELIX	217 221
FT	TURN	222 223
FT	STRAND	229 229
FT	HELIX	233 243
FT	TURN	244 244
FT	HELIX	247 249
FT	TURN	250 250
FT	TURN	253 254
Q -> QGVHGLVEMOTSKQILCRPAGDAHEHTVGAQGBELPC		
PVGVEAFARDINRAQPCR (In isoform 2).		
/FTId=VSP_002738.		
R -> W (in Ref. 1 and 2).		
Y -> I (in Ref. 2).		

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FT STRAND : 256 263
PT HELIX : 274 276

Query Match      100.0%; Score 6106; DB 1; Length 1170;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSCITWAMALLSGFFFPASSYNLDVRGASFPSPRARHGRYRLQVNGNYIGA 60
DB 1 MDSCITWAMALLSGFFFPASSYNLDVRGASFPSPRARHGRYRLQVNGNYIGA 60
QY 61 PEEGNSGSLYOCOSGTHCLPVTLRGSNYTSKYLGMTLATPTDGSILACDPSRTCD 120
DB 61 PEEGNSGSLYOCOSGTHCLPVTLRGSNYTSKYLGMTLATPTDGSILACDPSRTCD 120
QY 121 QNTYLSGLCYLFRONLQGFMLQGRPGQECIKGNVDFELFDGSMSLQDEFOKILDFMK 180
DB 121 QNTYLSGLCYLFRONLQGFMLQGRPGQECIKGNVDFELFDGSMSLQDEFOKILDFMK 180
QY 181 DVMKLTSTSYCPAAVQSTSYKTEFSDYKRCOPDALLKHYKMLLNTTFCALINY 240
DB 181 DVMKLTSTSYCPAAVQSTSYKTEFSDYKRCOPDALLKHYKMLLNTTFCALINY 240
QY 241 DVMKLTSTSYCPAAVQSTSYKTEFSDYKRCOPDALLKHYKMLLNTTFCALINY 240
DB 241 DVMKLTSTSYCPAAVQSTSYKTEFSDYKRCOPDALLKHYKMLLNTTFCALINY 240
QY 301 KFAKRPASEFVKILDTPEKLDLFTLEOKKIVIEGTSKODLTSFMELSSSGISADLSR 360
DB 301 KFAKRPASEFVKILDTPEKLDLFTLEOKKIVIEGTSKODLTSFMELSSSGISADLSR 360
QY 361 CHAVVGAAGKAWAGGFLDKADLDDDTFIGNEBLTPRYAGYLGTTWTLPBROKTSIL 420
DB 361 CHAVVGAAGKAWAGGFLDKADLDDDTFIGNEBLTPRYAGYLGTTWTLPBROKTSIL 420
QY 421 ASGARBYOMHGRVLLFOEPGOGGSHMSOVOTHTGTOIGSFEGELGVUNVDODGTELLLI 480
DB 421 ASGARBYOMHGRVLLFOEPGOGGSHMSOVOTHTGTOIGSFEGELGVUNVDODGTELLLI 480
QY 481 ASGARBYOMHGRVLLFOEPGOGGSHMSOVOTHTGTOIGSFEGELGVUNVDODGTELLLI 480
DB 481 ASGARBYOMHGRVLLFOEPGOGGSHMSOVOTHTGTOIGSFEGELGVUNVDODGTELLLI 480
QY 541 GAFLPYGBOGRGRVFIYORROLGFEEVESELQDPCYPLGRFEGATLALTDINGDLAVYA 540
DB 541 GAFLPYGBOGRGRVFIYORROLGFEEVESELQDPCYPLGRFEGATLALTDINGDLAVYA 540
QY 541 GAFLPYGBOGRGRVFIYORROLGFEEVESELQDPCYPLGRFEGATLALTDINGDLAVYA 540
DB 541 GAFLPYGBOGRGRVFIYORROLGFEEVESELQDPCYPLGRFEGATLALTDINGDLAVYA 540
QY 601 VCAESOMIVLASRPVVDWVTLMSFSPARIPVHEVSCYSTSKMKKEGVNITTCPOIKSLY 660
DB 601 VCAESOMIVLASRPVVDWVTLMSFSPARIPVHEVSCYSTSKMKKEGVNITTCPOIKSLY 660
QY 661 VCAESOMIVLASRPVVDWVTLMSFSPARIPVHEVSCYSTSKMKKEGVNITTCPOIKSLY 660
DB 661 VCAESOMIVLASRPVVDWVTLMSFSPARIPVHEVSCYSTSKMKKEGVNITTCPOIKSLY 660
QY 720 POFOGRVLANVLTTLQDLGHRTRRRGLFPQGRHELRNIAVTTSMSCDTDFSHFPVCOD 720
DB 720 POFOGRVLANVLTTLQDLGHRTRRRGLFPQGRHELRNIAVTTSMSCDTDFSHFPVCOD 720
QY 720 POFOGRVLANVLTTLQDLGHRTRRRGLFPQGRHELRNIAVTTSMSCDTDFSHFPVCOD 720
DB 720 POFOGRVLANVLTTLQDLGHRTRRRGLFPQGRHELRNIAVTTSMSCDTDFSHFPVCOD 720
QY 780 LISPIVNSLNSLWEEBEGTPRDQRAQKDIPIILAPSLHSTWEIIPFEKNCGEKCKCAN 780
DB 780 LISPIVNSLNSLWEEBEGTPRDQRAQKDIPIILAPSLHSTWEIIPFEKNCGEKCKCAN 780
QY 840 LRVSPSPARSRLRLTAFAASLSELSLNLBEDAWVQDLDFPPGSLFRKXEMLKPSQ 840
DB 840 LRVSPSPARSRLRLTAFAASLSELSLNLBEDAWVQDLDFPPGSLFRKXEMLKPSQ 840
QY 840 LRVSPSPARSRLRLTAFAASLSELSLNLBEDAWVQDLDFPPGSLFRKXEMLKPSQ 840
DB 840 LRVSPSPARSRLRLTAFAASLSELSLNLBEDAWVQDLDFPPGSLFRKXEMLKPSQ 840
QY 900 IPVSCCELPEESRLSLRALSQVSPPIFKAHSVALQMMFNTLVSSSGDSVELANVC 900
DB 900 IPVSCCELPEESRLSLRALSQVSPPIFKAHSVALQMMFNTLVSSSGDSVELANVC 900
QY 900 IPVSCCELPEESRLSLRALSQVSPPIFKAHSVALQMMFNTLVSSSGDSVELANVC 900
DB 900 IPVSCCELPEESRLSLRALSQVSPPIFKAHSVALQMMFNTLVSSSGDSVELANVC 900
QY 960 INHDIPTLEAVGVGPPESEPTIHWMSVQMEPPVPCHYEDLERLPDAAPCPCLGALFR 1020
DB 960 INHDIPTLEAVGVGPPESEPTIHWMSVQMEPPVPCHYEDLERLPDAAPCPCLGALFR 1020

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DB 961 INHDIPTLEAVGVGPPESEPTIHWMSVQMEPPVPCHYEDLERLPDAAPCPCLGALFR 1020
QY 1021 CPVVFROEILVQVIGTLELVEIEIENASSMFSLCSSLSISFNSSKPHLYGNSASLAQVYMK 1080
DB 1021 CPVVFROEILVQVIGTLELVEIEIENASSMFSLCSSLSISFNSSKPHLYGNSASLAQVYMK 1080
QY 1081 VDVIYKQMLLYLVLSGIGLILLLLIFIVLYKXGFPFRNLKEKWEAGRGVNGIPADS 1140
DB 1081 VDVIYKQMLLYLVLSGIGLILLLLIFIVLYKXGFPFRNLKEKWEAGRGVNGIPADS 1140
QY 1141 EQLASGQAGDPGCLKPLHEKDSGSGGKD 1170
DB 1141 EQLASGQAGDPGCLKPLHEKDSGSGGKD 1170

RESULT 2
ID 096HB1 PRELIMINARY; PRT, 1086 AA.
AC 096HB1
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ITGAL protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alech S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Kryzhanek M.I., Skalski U., Smalheiser D.B., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the Integrin alpha chain family.
EMBL: BC008777; AH08777.1; -.
HSSP: P20701.10GQ.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0008305; C:Integrin complex; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0007160; P:cell-matrix adhesion; IEA.
DR GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro: IPR000413; Integrin_alpha.
DR InterPro: IPR002035; VWP_A.
DR Pfam: PF00357; Integrin_alpha.1.
DR Pfam: PF00092; VWA.1.
DR PRINTS: PRO1185; INTEGRINA.
DR PRINTS: PRO0453; VWPADOMAIN.
DR SMART: SM00191; Int_alpha.5.
DR SMART: SM00327; VWA.1.

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DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VFMA; 1.  
 KW Cell adhesion; Integrin; Transmembrane.  
 SQ SEQUENCE 1086 AA; 119223 MW; F6F2546E8C632F9 CRC64;

Query Match 91.5%; Score 5585; DB 2; Length 1086;  
 Best Local Similarity 92.7%; Pred. No. 0;  
 Matches 1085; Conservative 0; Mismatches 1; Indels 84; Gaps 2;

QY 1 MKDCITVMAMALLSGFFFPAPASSYNLDVVGARSFSPRRGRHGVYLVQVGVYVGA 60  
 DB 1 MKDCITVMAMALLSGFFFPAPASSYNLDVVGARSFSPRRGRHGVYLVQVGVYVGA 60  
 QY PGEENSTSLYQOCOSGTGHCPTVTLRGSNYSKYLGMTLADPTDGTSLACDPGLSRCTD 120  
 DB PGEENSTSLYQOCOSGTGHCPTVTLRGSNYSKYLGMTLADPTDGTSLACDPGLSRCTD 120  
 QY 61 PGEENSTSLYQOCOSGTGHCPTVTLRGSNYSKYLGMTLADPTDGTSLACDPGLSRCTD 109  
 DB 61 PGEENSTSLYQOCOSGTGHCPTVTLRGSNYSKYLGMTLADPTDGTSLACDPGLSRCTD 109  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGQECIKGNVDLVFLFDGSMSLQPDFOKILDFMK 180  
 DB 110 ----- 109  
 QY 181 DVMKLSTNTSYQFAVQFSTSYKTEPDESDYVKRDPALLKHYKMLLTNTGAINVY 240  
 DB 110 -----FAVQFSTSYKTEPDESDYVKRDPALLKHYKMLLTNTGAINVY 157  
 QY 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAAKDIIRYIIGIGHFQTKESQETLH 300  
 DB 158 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAAKDIIRYIIGIGHFQTKESQETLH 217  
 QY 301 KFAKSPASEPVKIIDTFEKLKDLFTELQKIIYIEIGTSKODLTSPFMELSSSGISADLSR 360  
 DB 218 KFAKSPASEPVKIIDTFEKLKDLFTELQKIIYIEIGTSKODLTSPFMELSSSGISADLSR 277  
 QY 361 GHAVVAGVAGADMVAGFLDLKADLQDDPFIGNBPLTEPVKAGYLYTWTMLPSRQKTSLL 420  
 DB 278 GHAVVAGVAGADMVAGFLDLKADLQDDPFIGNBPLTEPVKAGYLYTWTMLPSRQKTSLL 337  
 QY 421 ASGAPRYOHMRGVLLFOEPQGGHWSQYQTHIGTQIGYFGGELCGVVDVDDGETELLII 480  
 DB 338 ASGAPRYOHMRGVLLFOEPQGGHWSQYQTHIGTQIGYFGGELCGVVDVDDGETELLII 397  
 QY 481 GAPIFYGEORGRVFIYQRRQLGFEEVSELQDPPGYLGRFGAETALTLDINGDGLVDVA 540  
 DB 398 GAPIFYGEORGRVFIYQRRQLGFEEVSELQDPPGYLGRFGAETALTLDINGDGLVDVA 457  
 QY 541 VGAPLEBEGGAVYIFNGRHGGLSPQPSQRIEQTQVLSGIQWFGRSIHGVYDLEBGDLADVA 600  
 DB 458 VGAPLEBEGGAVYIFNGRHGGLSPQPSQRIEQTQVLSGIQWFGRSIHGVYDLEBGDLADVA 517  
 QY 601 VGASQMTVLSRPVVDWTLMSPFPAEIPVHEVCSYSTSNKMGVNTICFOIKSLY 660  
 DB 518 VGASQMTVLSRPVVDWTLMSPFPAEIPVHEVCSYSTSNKMGVNTICFOIKSLY 577  
 QY 661 POFQGRVLANTYTLQLDGHRTRRRGLFPGGRHBLRNIATVTSMSCTDFSHPFVQVD 720  
 DB 578 POFQGRVLANTYTLQLDGHRTRRRGLFPGGRHBLRNIATVTSMSCTDFSHPFVQVD 637  
 QY 721 LISPIVNSLNTSWEESTPRDQAGNDIPPIILRSLHSETWEIPEFRKNGCEBKCCAN 780  
 DB 638 LISPIVNSLNTSWEESTPRDQAGNDIPPIILRSLHSETWEIPEFRKNGCEBKCCAN 696  
 QY 781 LRVFSFPARSRLRLTAPASLSVELSLNLEDAVWOLDLHFPFGLFRKYMCKPSPQ 840  
 DB 697 LRVFSFPARSRLRLTAPASLSVELSLNLEDAVWOLDLHFPFGLFRKYMCKPSPQ 756  
 QY 841 IPVSCBELLPEERSRLISRALSCNVSSPIFKAGSHVALQWMTLVNNSMGDSVELHANTYC 900  
 DB 757 IPVSCBELLPEERSRLISRALSCNVSSPIFKAGSHVALQWMTLVNNSMGDSVELHANTYC 816  
 QY 901 NNEDSDLEDNSATTTIPIILYPINLIDQDSDSTLYSFTFKGPKIHQVKMYQVRIOPS 960  
 DB 817 NNEDSDLEDNSATTTIPIILYPINLIDQDSDSTLYSFTFKGPKIHQVKMYQVRIOPS 876

QY 961 IHDHNIPTLEAVVGPVPPSESGPIITHQMSVQMEPPVPCHEYDELRUPDAEPCLPGALFR 1020  
 DB 877 IHDHNIPTLEAVVGPVPPSESGPIITHQMSVQMEPPVPCHEYDELRUPDAEPCLPGALFR 936  
 QY 1021 CPVVFROEIIIVQYITGTELVEIBASMFSLCSLSISFNSSKGFHLVGSNASTLAQVVMK 1080  
 DB 937 CPVVFROEIIIVQYITGTELVEIBASMFSLCSLSISFNSSKGFHLVGSNASTLAQVVMK 936  
 QY 1081 VDVVYERKQMLYLYVLSGIGLILLLLIFILYLVYVGFPRKRLKEKMEAGRGVPNGIPADS 1140  
 DB 997 VDVVYERKQMLYLYVLSGIGLILLLLIFILYLVYVGFPRKRLKEKMEAGRGVPNGIPADS 1056  
 QY 1141 EQLASQGEADPGCLXPEHKEKDESGGCKD 1170  
 DB 1057 EQLASQGEADPGCLXPEHKEKDESGGCKD 1086

RESULT 3  
 ITAL BOVIN STANDARD; PRT; 1165 AA.  
 AC P61625;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha chain) (CD11a).  
 DE Name=ITGAL;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14697514; DOI=10.1016/j.gene.2003.09.043;  
 RA Felt T., Zecchion L., Baise E., Desmecht D.;  
 RT "The bovine (Bos taurus) CD11a-encoding cDNA: molecular cloning, characterisation and comparison with the human and murine glycoproteins".  
 RT Gene 325:97-101(2004).  
 RL Gene 325:97-101(2004).  
 CC -1- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2, ICAM3 and ICAM4. It is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes and monocytes (By similarity).  
 CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L associates with beta-2 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -1- DOMAIN: The integrin I-domain (insert) is a VFMA domain. Integrins with I-domains do not undergo protease cleavage.  
 CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
 CC -1- SIMILARITY: Contains 7 FG-GAP repeats.  
 CC -1- SIMILARITY: Contains 1 VFMA domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL; AY267467; AB994035.1; -  
 DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VFMA; 1.  
 KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 23  
 FT CHAIN 24 1165  
 FT DOMAIN 24 1084  
 FT TRANSMEM 1085 1105  
 FT DOMAIN 1106 1165  
 FT POTENTIAL 1165  
 FT CYTOPLASMIC 1165



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FT REPEAT 40 88 FG-GAP 1.
FT REPEAT 89 146 FG-GAP 2.
FT DOMAIN 153 324 VMPA.
FT REPEAT 347 397 FG-GAP 3.
FT REPEAT 398 452 FG-GAP 4.
FT REPEAT 454 513 FG-GAP 5.
FT REPEAT 515 572 FG-GAP 6.
FT REPEAT 575 627 FG-GAP 7.
FT CA_BIND 465 473 Potential.
FT CA_BIND 527 535 Potential.
FT CA_BIND 587 595 Potential.
FT SITE 1111 1115 GEFKR motif.
FT DISULFID 71 78 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 650 704 By similarity.
FT DISULFID 768 774 By similarity.
FT DISULFID 842 858 By similarity.
FT DISULFID 994 1009 By similarity.
FT DISULFID 1017 1048 By similarity.
FT CARBOHYD 33 33 N-linked (GlcNAc...) (potential).
FT CARBOHYD 86 86 N-linked (GlcNAc...) (potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (potential).
FT CARBOHYD 646 646 N-linked (GlcNAc...) (potential).
FT CARBOHYD 667 667 N-linked (GlcNAc...) (potential).
FT CARBOHYD 723 723 N-linked (GlcNAc...) (potential).
FT CARBOHYD 859 859 N-linked (GlcNAc...) (potential).
FT CARBOHYD 894 894 N-linked (GlcNAc...) (potential).
FT CARBOHYD 929 929 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1056 1056 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1067 1067 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 1165 AA; 128725 MW; DAEB3A3F1E1463CB CRC64;

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Query Match 76.3%; Score 4657.5; DB 1; Length 1165;  
 Best Local Similarity 77.3%; Pred. No. 1.7e-297;  
 Matches 901; Conservative 98; Mismatches 164; Indels 3; Gaps 3;

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QY 3 DSCIVVMALISGFFFPASSYVLVDRGASFPSPAPRGVYGVNGVYVAGP 62
DB 2 NSCIIVLRI-LISGPFVPAWVSYNLVDVHVNQFSPLAGRHFYGVYVQVGGVVGAPS 60
QY 63 EGNSTGSLYQCGSTGHCPLVTLRGSNTSKYLGWTLATDPTDGSILACDPLSRPCON 122
DB 61 EGNMGNLYQCGPEIGDCPLVTL-SSNTSKYLGWTLATDPTDGLACDPLSRPCON 119
QY 123 TYLSGLCYLFRQNLQCPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFOKIILPMKV 182
DB 120 TYLSGLCYLIHNLGHPVQLQGHGPGYQECIKGNVDLVFLFDGSMSLQDPDFOKIILPMKV 179
QY 183 MKKLSNTSYQPAANQFSTSYKTEPSPDYVVRKDDALIKAYKMLLTNTFGAINVAT 242
DB 180 MKKLSNTSYQPAANQFSTSYKTEPSPDYVVRKDDALIKAYKMLLTNTFGAINVAT 239
QY 243 EYFRELIGARPATVLIITITGATDSGNIDAAIDIIIRYIIIGIKHPTKESQSTLKF 302
DB 240 EYFRELIGARPATVLIITITGATDSGNIDAAIDIIIRYIIIGIKHPTKESQSTLKF 299
QY 303 ASKPASFEVKILDTFEKLDLTELQKTIYVIEGTSKDLTSFNNELSSSGISADLSRGH 362
DB 300 ASKPASFEVKILDTFEKLDLTELQKTIYVIEGTSKDLTSFNNELSSSGISADLSRGH 359
QY 363 AVYGVAVKADWAGSLDLDKADLDQDTFIGNEPLEFEVAVAGYIGYVTVLPSKQKTSLLA 422
DB 360 GYGVAVKADWAGSLDLDKADLDQDTFIGNEPLEFEVAVAGYIGYVTVLPSKQKTSLLA 419
QY 423 GAPRYOHGRRVLLFQPKRGKSGWISQIQRIDGQISYFGELCGVDVBDGETELLILA 482
DB 420 GAPRYOHGRRVLLFQPKRGKSGWISQIQRIDGQISYFGELCGVDVBDGETELLILA 479
QY 483 PLFYGEORGRVYIYORRQLGFEVSELOGBDGYPLGRFGAITALTIDNGDLVAVAG 542
DB 480 PLFYGEORGRVYIYORRQLGFEVSELOGBDGYPLGRFGAITALTIDNGDLVAVAG 539
QY 543 APLBEOGAVYIFNGHGGSLSPQSRIGSTQVLSGIQFGRSHGVKDLGDLADVAVG 602

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DB 540 APLBEOGAVYIFNGHGGSLSPQSRIGSTQVLSGIQFGRSHGVKDLGDLADVAVG 599
QY 603 AESQWIVLSRPVYDMVTLMSFSPAELPVHEVECSYSTSNKMGVNTTICFOIKSLYPQ 662
DB 600 AEGQIVLSRPVYDMVTLMSFSPAELPVHEVECSYSTSNKMGVNTTICFOIKSLIST 659
QY 663 FQGRVAVLTTTLQDGRTRRGLFPGGRHLELRNIAVTTSMGCTDSSFFPVCVDLI 722
DB 660 FQGRVAVLTTTLQDGRTRRGLFPGGRHLELRNIAVTTSMGCTDSSFFPVCVDLI 719
QY 723 SPINVLNFSLMBEGTFRDQAOQKQIPILRPSLSHSETWEIPREKKGCDKCEANLR 782
DB 720 SPINVLNFSLMBEGTFRDQAOQKQIPILRPSLSHSETWEIPREKKGCDKCEANLR 779
QY 783 VSPFARSRALRLTAPASLVELSLSNLEBDAYVVOULHPPGLSFRKEMLKPHSQIP 842
DB 780 LAFSDMRSKIRLTPSASLVELSLSNLEBDAYVVOULHPPGLSFRKEMLKPHSQIP 839
QY 843 VSCBELPESRLSRLASCNVSPILFKAHSHVALQMFNTLVNSWGDVSELHANTQNN 902
DB 840 VSCBELPESRLSRLASCNVSPILFKAHSHVALQMFNTLVNSWGDVSELHANTQNN 899
QY 903 EDSULLENSATTTIPIIYPIINILIQDQDSTLVVSPFKGPKTHQVAMTVORIPSII 962
DB 900 EDSULLENSATTTIPIIYPIINILIQDQDSTLVVSPFKGPKTHQVAMTVORIPSII 959
QY 963 DNIPTLEAVVQDPPSEGPITTHQVSVOMEPVPCYHEDLERLDAAPCLPGALFPCP 1022
DB 960 DNIPTLEAVVQDPPSEGPITTHQVSVOMEPVPCYHEDLERLDAAPCLPGALFPCP 1018
QY 1023 VVFEQELIVQYIGLELVGRIEASMSFSLCSLSISFNSSGHFHLVGSNASLAQVYMKVD 1082
DB 1019 VVFEQELIVQYIGLELVGRIEASMSFSLCSLSISFNSSGHFHLVGSNASLAQVYMKVD 1078
QY 1079 LVYERKMLYLVLSGIGGLLILFLIYLVYVGPKNLKEKMGARVPGVPADESO 1142
DB 1076 LVYERKMLYLVLSGIGGLLILFLIYLVYVGPKNLKEKMGARVPGVPADESO 1138
QY 1143 LASQGEAGDPCCLPLHEKDSRSGCG 1168
DB 1139 LASQGEAGDPCCLPLHEKDSRSGCG 1164

```

RESULT 4  
 OCTYB8 PRELIMINARY; PRT; 1166 AA.  
 ID OCTYB8  
 AC OCTYB8.  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Lymphocyte function-associated antigen 1 alpha subunit CD1A.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RA Dileepan T., Thumthik P., Kannan M.S., Maheswaran S.K.;  
 RL Submitted (SEP-2003) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
 DR EMBL; AY382558; AAC90015.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0068305; C:integral complex; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0007160; P:cell-matrix adhesion; IEA.  
 DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.  
 DR InterPro; IPR000413; Integrin\_alpha.  
 DR Pfam; PF01839; FG-GAP; 3.  
 DR Pfam; PF00357; Integrin\_alpha; 1.

DR Pfam; PF00092; VWA; 1.  
 DR PRINTS; PR01185; INTEGRINA.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR SMART; SM00181; Int\_alpha; 5.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VWA; 1.  
 KW Cell adhesion; Integrin; Transmembrane.  
 SQ SEQUENCE 1166 AA; 128723 MW; 78BD8AFBA896C9DF CRC64;

Query Match 74.9%; Score 4571.5; DB 2; Length 1166;  
 Best Local Similarity 75.9%; Pred. No. 8e-292;  
 Matches 886; Conservative 103; Mismatches 176; Indels 3; Gaps 3;

QY 1 MKDCITIMAMALLSGFFFPASSYNLDVNGARSPSPRAGRHHGYVLDVNGVNYGA 60  
 DB 1 MKDCITIALRL-LISGPFVFAFAMSYNLDVHVNQFSPFLGRHGYVLDVNGVNVGA 59  
 QY PEGNSTSLVYOCOSGTGHCPLVTLRGSNYTSKYLGMTLATDPTDGSILACDPGLSRTCD 120  
 DB PSEGNMKNLYOCQPEITDCLPVTL-SSNYTSKYLGMTLATDPTSDNLACDPGLSRTCD 118  
 QY 121 QNTYLSGLCYLFRONTLOGPMLQGRPGFQECIKGNVDVLFDFGSMISLPDEFQKILDFMK 180  
 DB 119 QNTYLSGLCYLIHEHRLGVPVQLQHHPGYQECIKGNVDVLFDFGSMISLPDEFQKILDFMK 178  
 QY 181 DVMKLSTSYQFAAVOSTSYKTEPDSYVKRDPDALLKHYKGMILLNTTGCALNYV 240  
 DB 179 DVMKLSTSYQFAAVOSTSYKTEPDSYVKRDPDALLKHYKGMILLNTTGCALNYV 238  
 QY 241 ATEVFRBELGARPDAATKYLIIITDGEATDSGNIADAKDIIKIIIGISGHFQTKESQETLH 300  
 DB 239 AKETVFRPDLGARPDATKYLIIITDGEATDSGNIADAKDIIKIIIGISGHFQTKESQETLH 298  
 QY 301 KFAKPDASEFYKILDTFEKLKDLFTELQKIIYVIGTSKODLTSPFMELSSSGISADLSR 360  
 DB 299 QFAKPDASEFYKILDTFEKLKDLFTELQKIIYVIGTSKODLTSPFMELSSSGISADLSR 358  
 QY 361 GHAVANGAGADMAGGFLDILADLDDPFIGNEPILTEPVRAKYLGYTWTMLPSRKSTLL 420  
 DB 359 GHGVGAGADMAGGFLDILADLDDPFIGNEPILTEPVRAKYLGYTWTMLPSRKSTLL 418  
 QY 421 ASGAPRYOMGRVLLFQEPQSGHMSQVQTHGTIGISYFGGELCGVVDODGETELLII 480  
 DB 419 ATGAPRYOMGRVLLFQEPQSGHMSQVQTHGTIGISYFGGELCGVVDODGETELLII 478  
 QY 481 GAPPFYEGORGRVFIYRROLGFESEVELQDGPYPLGRFGELATLTALTDINGDLVDVA 540  
 DB 479 AAPFYEGORGRVFIYRROLGFESEVELQDGPYPLGRFGELATLTALTDINGDLVDVA 538  
 QY 541 VGAPLEBEGAVYIFNGRHGGLSPQSORIEGTQVLSGIQWGRSITHGKDLLEGGLADVA 600  
 DB 539 VGAPLEBEGAVYIFNGRHGGLSPQSORIEGTQVLSGIQWGRSITHGKDLLEGGLADVA 598  
 QY 601 VGASQSMIVLSRPVVDWTLMSPFPAEIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
 DB 599 VGABEQVIVLSRPVVDITTSVSEBPAPIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 658  
 QY 661 POFQGRIVANTTYTLQDLGHRTRRRGLPPGGRHLELRNIAVTTNSCTDFSFHFPVQVD 720  
 DB 659 STFOGHIVANTTYTLQDLGHRTRRRGLPPGGRHLELRNIAVTTNSCTDFSFHFPVQVD 718  
 QY 721 LISPIVNSLNSLWEEBGTPRDQAGKODIPPIILPSLSHSEIWEIPEFKNGCEDKCCAN 780  
 DB 719 LISPIVNSLNSLWEEBGTPRDQAGKODIPPIILPSLSHSEIWEIPEFKNGCEDKCCAN 778  
 QY 781 LRVSPSPARSALRTAFAASIVELSLNLEDAVWVOLDLHPPGLSFRKYMKLKPPSQ 840  
 DB 779 LKLAFSDMRSKILRLITPSASISYRLTLNRTAEDAVWVYTLSPFGLSFRKYEILKPPSH 838  
 QY 841 IPVSCCELLPEBSRLLSRLASCNVSSPIFKAGHSVALQWMTLVNNSMGDSVELHANVTC 900  
 DB 839 VPVCGEELPEBAVHSRLASCNVSSPIFKAGHSVALQWMTLVNNSMGDSVELHANVTC 898

QY 901 NNEDSDLENNASATTIPIILYINILIQOEDSTLYVSFTPKGPKIHQWAMYOVRIOPS 960  
 DB 899 NNEDSDLENNASATTIPIILYINILIQOEDSTLYVSFTPKGPKIHQWAMYOVRIOPS 958  
 QY 961 IHDNIPFLBAVVGVPQSPSEGPITTHQMSVQMEPPVPCHEYDLERLPDAAPCLPGALFR 1020  
 DB 959 NYD-NMPPLEALVVRPVHSEGLITHKMSIQMEPPVPCSPRNLESPSDEASCFTGEFR 1017  
 QY 1021 CPVYFRQELIVQYITGIELVGEIBASSMBSLCSLSISFNSSKHFHLVGSNASIAQVYMK 1080  
 DB 1018 CPIDFRQELIIVQVQWGWELKGTIKASSMSLSLCSLAIISFNSSKHFHLVGSNASIAQVYMK 1077  
 QY 1081 VDVYKEMKLYLYVLSGIGLLILLIFLYLYKVPFKRNLKEMKEMAGRGVNGIPEADS 1140  
 DB 1078 VDLVYKEMKLYLYVLSGIGLLILLIFLYLYKVPFKRNLKEMKEMAGRGVNGIPEADS 1137  
 QY 1141 EQLASQEGADPGCLKPLHEKDSGSGG 1168  
 DB 1138 GQPELBKCKDPSCLBPLNHTDDEGSGG 1165

RESULT 5  
 Q9WTV4  
 AC Q9WTV4; PRELIMINARY; PRT; 1161 AA.  
 DT 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
 DE Integrin alpha L.  
 GN Name=Itgal;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DRA/2J; TISSUE=spleen;  
 RA Ma R.Z., Teuscher C.,  
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
 DR EMBL; AF065902; AAD25885.1; -.  
 DR HSSP; P20701; IDGO.  
 DR MED; MG1.96506; Itgal.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR InterPro; IPR000413; Integrin\_alpha.  
 DR InterPro; IPR02035; VWF\_A.  
 DR Pfam; PF00357; FG-GAP; 1.  
 DR Pfam; PF00357; Integrin\_alpha; 1.  
 DR Pfam; PF00092; VWA; 1.  
 DR PRINTS; PR00453; INTEGRINA.  
 DR PRINTS; PR01185; INTEGRINA.  
 DR SMART; SM00191; Int\_alpha; 5.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VWA; 1.  
 KW Cell adhesion; Integrin; Transmembrane.  
 SQ SEQUENCE 1161 AA; 128240 MW; 86B102F7B209E431 CRC64;

Query Match 71.5%; Score 4365.5; DB 2; Length 1161;  
 Best Local Similarity 72.6%; Pred. No. 3e-278;  
 Matches 839; Conservative 124; Mismatches 185; Indels 7; Gaps 6;

QY 13 LISGPFPPAPASSYNLDVNGARSPSPRAGRHHGYVLDVNGVNYGAPEGNSTGSLYQ 72  
 DB 11 LISGPFPPAPASSYNLDVNGARSPSPRAGRHHGYVLDVNGVNYGAPEGNSTGSLYQ 69  
 QY 73 CQSGTGHCLPVTLRGNSYTSKYLGMTLATDPTDGSILACDPGLSRTCDONTYLSGLCYLP 132  
 DB 70 CRTSSEFCQPVSLIGSNHSTSKYLGMTLATDPAAGSILACDPGLSRTCDONTYLSGLCYLP 129

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QY 133 RQNLQPMLOQRPGFOECIKGNVDFLPDGSMSLOPDEFOKILDPMDKWKLSNTSYQ 192
DB 130 PGLSGPMLQNRPAVOECMKGVDFLPDGSQSLDRKDFEKILEPMDVWKLSNTSYQ 189
QY 193 PAAVOFSTSYKTEPFDSDYVR-KDPDALLKHVKMLLTNTFGAINVATEVFEELGA 251
DB 190 PAAVOFSTDCRTEPFLDYVQKNKPDVLLGSVQPMFLTNTFPAINVVAHVFEBSGA 249
QY 252 RPDATKVLITITDGEATDSGNIDAAKDIRITIGIKGFQTESQETLHKPASKPASEFV 311
DB 250 RPDATKVLITITDGEATDSGNISAAHDIRITIGIKGFVSVQOKTILHIFASEPVEEFV 309
QY 312 KIUDPEKLDLPTELQKKIYVIBGTSKODLTSFPMELSSSGISADLSRGHVGAVGAK 371
DB 310 KIUDPEKLDLPTELQKKIYVIBGTSKODLTSFPMELSSSGISADLSRGHVGAVGAK 369
QY 372 DWAGFLDLKADLDDDTFIGNEPILPEVYAGYLTWTLPOROKTSLASGAPRYOHMG 431
DB 370 DWAGFLDLKADLDDDTFIGNEPILPEVYAGYLTWTLPOROKTSLASGAPRYOHMG 429
QY 432 RVLLFOEPQGGHWSQVQTIHGTOIGSYFGGELCGVNDVQDETELLILGAPLYGBOG 491
DB 430 RVLLFOEPQGGHWSQVQTIHGTOIGSYFGGELCGVNDVQDETELLILGAPLYGBOG 489
QY 492 GRVFTYORRQGLFEVSELOQDPGYPLGRFGAITALTDINDGLVDAVGAHLEGGAV 551
DB 490 GRVFTYORRQGLFEVSELOQDPGYPLGRFGAITALTDINDGLVDAVGAHLEGGAV 549
QY 552 YIFNGRHGLSPQSPORIEGTQVLSGIOMFGSHIGVNDLEBDGLADVAGASQOMVLS 611
DB 550 YIFNGRHGLSPQSPORIEGTQVLSGIOMFGSHIGVNDLEBDGLADVAGASQOMVLS 609
QY 612 SRPVDVMTWLSFSPAPLPEVHEVCSYSTSNMKGAVNTTCFOIKSLYPOQRLVANT 671
DB 610 SRPVDVMTWLSFSPAPLPEVHEVCSYSTSNMKGAVNTTCFOIKSLYPOQRLVANT 669
QY 672 TYTLODGRTRRGLFPGGRHLEKRNIAVTTSMCTDPSFHPVPCVQDLISPIVNSLNF 731
DB 670 TYTLODGRTRRGLFPGGRHLEKRNIAVTTSMCTDPSFHPVPCVQDLISPIVNSLNF 729
QY 732 SLMBEGFRPDORAOQKIDPILRPSLHSETWEIPFEKNCGBDKCEANTLRSFSPARS 791
DB 730 SLMBEGFRPDORAOQKIDPILRPSLHSETWEIPFEKNCGBDKCEANTLRSFSPARS 786
QY 792 ALRLTAFASLSVELSLNLEBDAYVQDLHPPGGLSFRKVMKPHSQIPVSCBELPE 851
DB 787 ALRLTAFASLSVELSLNLEBDAYVQDLHPPGGLSFRKVMKPHSQIPVSCBELPE 846
QY 852 SLLSRAISLSCVSPIFKAGHVALQAMPTLVNWSKGDVRLHANVTGNEDSLLBDN 911
DB 847 SLLSRAISLSCVSPIFKAGHVALQAMPTLVNWSKGDVRLHANVTGNEDSLLBDN 906
QY 912 SATTIIPILYPIINILIODEDSTLVSPFKGPKLHOVMKYOVRLOPSIHNDHPTLEA 971
DB 907 SATTIIPILYPIINILIODEDSTLVSPFKGPKLHOVMKYOVRLOPSIHNDHPTLEA 966
QY 972 VVGVPQPSBEGPITQWVSQVMEPVPVCHYEDLER-LPDAABPCLPGALFRCPVREOETL 1030
DB 967 VVGVPQPSBEGPITQWVSQVMEPVPVCHYEDLER-LPDAABPCLPGALFRCPVREOETL 1026
QY 1031 VOYITGLBVGIEKMSMFLSCSSLSISFNSSKPHLYGSNLSLAQVNMKVDVTEKQML 1090
DB 1027 VOYITGLBVGIEKMSMFLSCSSLSISFNSSKPHLYGSNLSLAQVNMKVDVTEKQML 1086
QY 1091 VYVYLSGIGGLLLILFIVLYKVPFKKNLKKMKBAGRGVNGAI PAEDSEOLA-SGORA 1149
DB 1087 VYVYLSGIGGLLLILFIVLYKVPFKKNLKKMKBAGRGVNGAI PAEDSEOLA-SGORA 1146
QY 1150 GDPGLCKPLHKKDSE 1164
DB 1147 KDMGCLPLRBSDKD 1161

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RESULT 6
Q9R200 ID Q9R200 PRELIMINARY; PRT; 1160 AA.
AC Q9R200;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Integrin alpha L.
GN Name:Itgal;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spleen;
RA Ma R.Z., Teuscher C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-1- SIMILARITY: Belongs to the Integrin alpha chain family.
DR EMBL; AF065901; AAD25884.1; -.
DR HSSP; P20701; IDQO.
DR MGD; MGI:96606; Itgal.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR00413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; Fg-GAP; 1.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWFA; 1.
KM Cell adhesion; Integrin; transmembrane.
SQ SEQUENCE 1160 AA; 128127 MW; A33C531B139F1PAD CRC64;

Query Match 71.4%; Score 4361; DB 2; Length 1160;
Best Local Similarity 72.6%; Pred. No. 5,8e-278;
Matches 838; Conservative 123; Mismatches 187; Indels 6; Gaps 5;
QY 13 ILSGFFPAPASSYINLVDRGARSFSPPRAGHFGYRLVQVNGVIVGAPGEGNSTGSLYQ 72
DB 11 LLLGLQPAKAMSYNLDTRPQSF-L-AQAGHFGYQVLQIDGVVVGAPGEGDNTGGLYH 69
QY 73 QSGTGHLPTYLGLSGNTSKYLGWTLATDPTDGSIIACDPGLSRTCDQNTYLSGLCYLF 132
DB 70 CRTSEFCQPVSLHGSNHTSKYLGWTLATDAAKGSLLACDPGLSRTCDQNTYLSGLCYLF 129
QY 133 RQNLQPMLOQRPGFOECIKGNVDFLPDGSMSLOPDEFOKILDPMDKWKLSNTSYQ 192
DB 130 PGLSGPMLQNRPAVOECMKGVDFLPDGSQSLDRKDFEKILEPMDVWKLSNTSYQ 189
QY 193 PAAVOFSTSYKTEPFDSDYVR-KDPDALLKHVKMLLTNTFGAINVATEVFEELGA 251
DB 190 PAAVOFSTDCRTEPFLDYVQKNKPDVLLGSVQPMFLTNTFPAINVVAHVFEBSGA 249
QY 252 RPDATKVLITITDGEATDSGNIDAAKDIRITIGIKGFQTESQETLHKPASKPASEFV 311
DB 250 RPDATKVLITITDGEATDSGNISAAHDIRITIGIKGFVSVQOKTILHIFASEPVEEFV 309
QY 312 KIUDPEKLDLPTELQKKIYVIBGTSKODLTSFPMELSSSGISADLSRGHVGAVGAK 371
DB 310 KIUDPEKLDLPTELQKKIYVIBGTSKODLTSFPMELSSSGISADLSRGHVGAVGAK 369
QY 372 DWAGFLDLKADLDDDTFIGNEPILPEVYAGYLTWTLPOROKTSLASGAPRYOHMG 431
DB 370 DWAGFLDLKADLDDDTFIGNEPILPEVYAGYLTWTLPOROKTSLASGAPRYOHMG 429
QY 432 RVLLFOEPQGGHWSQVQTIHGTOIGSYFGGELCGVNDVQDETELLILGAPLYGBOG 491

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Db 430 QVLLFQAEAGAGRNQOTKIEGTQIGSYFPGELCSVDLDQDGEALLIGALFFEGEORG 489
Qy 492 GRVFIYORROLGFEEVSELOQDPGYPLARFGEATATLTDINDGGLVDVAVGAPLEEGAV 551
Db 490 GRVFIYORROLGFEEVSELOQDPGYPLARFGEATATLTDINDGGLVDVAVGAPLEEGAV 549
Qy 552 YIFNRRHGLSPQSPQSRIEGTVLSGIQMPGASIHGVKDLBGDLADYAVGASQMIYLS 611
Db 550 YIFNRRHGLSPQSPQSRIEGTVLSGIQMPGASIHGVKDLBGDLADYAVGAPLEEGAV 609
Qy 612 SRPVDMVTLMSFSPAEIPIVHEVECSYSTSNKMEGNVITTCFOIKSLYPPQGLVAVL 671
Db 610 SRPVDMVTLMSFSPAEIPIVHEVECSYSTSNKMEGNVITTCFOIKSLYPPQGLVAVL 669
Qy 672 TYTLQDLGHTRRRRRLFPFGGRHELRNIAVTTSMCTPFSFHPFVPCVODLSPINVSINF 731
Db 670 TYTLQDLGHTRRRRRLFPFGGRHELRNIAVTTSMCTPFSFHPFVPCVODLSPINVSINF 729
Qy 732 SLMEBEGTPRDOQAQKDIPIILRPSLHSEWEIPEKXNCGEDKCEANLAVSPSPARS 791
Db 730 SLMEBEGTPRDOQAQKDIPIILRPSLHSEWEIPEKXNCGEDKCEANLAVSPSPARS 786
Qy 792 ALRLTAFASVSELSTSLMEBDAVWVOLDLHPPRGLSPKXVEMLKPHSQIPVSCHELEEB 851
Db 787 PLRLMSASJLAVEMWTLNSGSDAYWRDLDPRLGLSPKXVEMLKPHSRMPVSCHELEEB 846
Qy 852 SRLLSRALSCNVSPSIFPAGHSVALQMMFNTLVNSGWDSEVLAHVYCNNEEDSLBDN 911
Db 847 SLLILKTKLKNVSPSIFPAGHSVALQMMFNTLVNSGWDSEVLAHVYCNNEEDSLBDN 906
Qy 912 SATTTIPLIYPIINIIQOEDSTLYVSTPKGPKTHQVEMVQVRIQPSIHDMNITPLEA 971
Db 907 SAATTHIPVLYPVNIIKTEQENSTLYISFTPKGPKTHQVEMVQVRIQPSIHDMNITPLEA 966
Qy 972 VVGVPQPSSEGPITQMSVQVMEPPVCHYBDELRDAAEPLTPEALRCPCVPRQETIV 1031
Db 967 LVGVPRPSEDLITITWVQDPLTTCSEBDEKRRSSAEPLCPVQPRCPVIFVFWELI 1026
Qy 1032 QVITGLTELVEIEASMFSLCSLSISFNSSKHFIYGSNNAIQAQVWKKVVDVYKQMLY 1091
Db 1027 QVTGVLVEISKEIKASSTLSCSLSVSPNSSKHFIYGSNNAIQAQVWKKVVDVYKQMLY 1086
Qy 1092 LYVLSGIGGLLLLIIFIVLYKVGFFKNLKEKMEAGRGVNGIIPAEDEQLA-SGQFAG 1150
Db 1087 VYVLSGIGGLVLIIFIVLYKVGFFKNLKEKMEAGRGVNGIIPAEDEQLA-SGQFAG 1146
Qy 1151 DPGCLXPLHEKDE 1164
Db 1147 DWGCLLEPRESDKD 1160

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RN [2]
RP SEQUENCE OF 24-42.
RX MEDLINE=85188276; PubMed=387182;
RA Springer T.A., Teplov D.B., Dreyer W.J.;
RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
RL glycoproteins and unexpected relation to leukocyte interferon.";
CC Nature 314:540-542(1985).
CC -1- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2,
CC ICAM3 and ICAM4. Is involved in a variety of immune phenomena
CC including leukocyte-endothelial cell interaction, cytotoxic T-cell
CC mediated killing, and antibody dependent killing by granulocytes
CC and monocytes. Mice expressing a null mutation of the alpha-L
CC subunit gene demonstrate impaired tumor rejection and impaired
CC leukocytes recruitment.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
CC associates with beta-2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Leukocytes.
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
DR EMBL; M60778; AAA39426.1; -.
DR PIR; I56126; I56126.
DR HSSP; P20701; IDQG.
DR MGD; MGI:96606; Itgal.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF01839; FG-GAP; 2.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWFA; 1.
DR PRINTS; PRO1185; INTEGRIN.
DR SMART; SM00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein;
KW Integrin; Magnesium; Receptor; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 1163
FT DOMAIN 24 1087
FT TRANSMEM 1088 1108
FT DOMAIN 1109 1163
FT REPEAT 39 88
FT REPEAT 89 146
FT DOMAIN 153 325
FT REPEAT 348 398
FT REPEAT 399 454
FT REPEAT 455 514
FT REPEAT 516 573
FT REPEAT 576 628
FT CA_BIND 466 474
FT CA_BIND 528 536
FT CA_BIND 588 596
FT SITE 1111 1115
FT DISULFID 70 77
FT DISULFID 108 126
FT DISULFID 147 199
FT DISULFID 651 705
FT DISULFID 767 773
FT DISULFID 840 856
FT DISULFID 993 1009

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FT DISULFID 1017 1048 By similarity.
FT CARBOHYD 86 86 N-linked (GlcNAc...) (potential)
FT CARBOHYD 185 185 N-linked (GlcNAc...) (potential)
FT CARBOHYD 270 270 N-linked (GlcNAc...) (potential)
FT CARBOHYD 444 444 N-linked (GlcNAc...) (potential)
FT CARBOHYD 668 668 N-linked (GlcNAc...) (potential)
FT CARBOHYD 696 696 N-linked (GlcNAc...) (potential)
FT CARBOHYD 724 724 N-linked (GlcNAc...) (potential)
FT CARBOHYD 728 728 N-linked (GlcNAc...) (potential)
FT CARBOHYD 776 776 N-linked (GlcNAc...) (potential)
FT CARBOHYD 857 857 N-linked (GlcNAc...) (potential)
FT CARBOHYD 880 880 N-linked (GlcNAc...) (potential)
FT CARBOHYD 890 890 N-linked (GlcNAc...) (potential)
FT CARBOHYD 899 899 N-linked (GlcNAc...) (potential)
FT CARBOHYD 927 927 N-linked (GlcNAc...) (potential)
FT CARBOHYD 1056 1056 N-linked (GlcNAc...) (potential)
SQ SEQUENCE 1163 AA; 128343 MW; A7A30784898232F CRC64;

Query Match
Best Local Similarity 71.1%; Score 4343.5; DB 1; Length 1163;
Matches 836; Conservative 123; Mismatches 182; Indels 7; Gaps 6;

QY 13 LLSGFFPAPASSYNLDVAGARSFSPRAGRHFGRVLOVNGVIVGAPGEGNSTGSLYQ 72
DB 11 LLLGLQLPKAKSYNLDLRPTQSLF-AQAGRHFQVQVQIBGVVVGAPGEGNDTGLYH 69
QY 73 CQSGTGHCLPVTLRGSSNTSKYLGMTLATDPTDSSILACDPGLSRTCDONTYLSGLCYLF 132
DB 70 CRTSEFPQVPVSLHSGSNHTSKYLGMTLATDAKGSILACDPGLSRTCDONTYLSGLCYLF 129
QY 133 RNLQGPMLQGRPGQECIKGNVDLVELFDGNSIQDFQKILDPMDVMKLSNTSYQ 192
DB 130 PQLSGPMLQNPAYQECIKGNVDLVELFDGNSIQDFQKILDPMDVMKLSNTSYQ 189
QY 193 FAAVQFSTSYKTEPFPSDYKVR-KDPDALIKVKNMLLTTFNGAINVYATVFREEGA 251
DB 190 FAAVQFSTDCRTEPFPSDYKVR-KDPDALIKVKNMLLTTFNGAINVYATVFREEGA 249
QY 252 RPDATKVLIIITGSAITSGNIDAKDIIIRYIIIGIKGFPQTKESQETLHKFASPKASBFV 311
DB 250 RPDATKVLIIITGSAITSGNIDAKDIIIRYIIIGIKGFPQTKESQETLHKFASPKASBFV 309
QY 312 KILDTFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSGSIADLSRGHNVAGVAK 371
DB 310 KILDTFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSGSIADLSRGHNVAGVAK 369
QY 372 DWAGGFLDLKADLQDPTFIGNBPLTPRYAGLYTWTWLPKROKTSLLASGAPRYOMG 431
DB 370 DWAGGFLDLKADLQDPTFIGNBPLTPRYAGLYTWTWLPKROKTSLLASGAPRYOMG 429
QY 432 RYLLFQEPQGGHWSQVOTIHGTQIGSYFGELGCVDDVDDGETELLIGAPLFYGEQNG 491
DB 430 RYLLFQEPQGGHWSQVOTIHGTQIGSYFGELGCVDDVDDGETELLIGAPLFYGEQNG 489
QY 492 GRVFIYQKROLGFEVSEIQLGDPGPIPLGFRGALITLTDINDGVLVAVGAPLEQAV 551
DB 490 GRVFIYQKROLGFEVSEIQLGDPGPIPLGFRGALITLTDINDGVLVAVGAPLEQAV 549
QY 552 YIFNGRHGGLSPQSORIEGTQVLSGIOWFGSHGVNDLEGGDLADVAVGASCOMYLS 611
DB 550 YIFNGRHGGLSPQSORIEGTQVLSGIOWFGSHGVNDLEGGDLADVAVGASCOMYLS 609
QY 612 SRPVVDWYTLMSFSPAEIPVHEVECSYSTSNKKEGVNITTCFOIKSLIYPOFQELVANT 671
DB 610 SRPVVDWYTLMSFSPAEIPVHEVECSYSTSNKKEGVNITTCFOIKSLIYPOFQELVANT 669
QY 672 TYTTLQDGRTRRRLGFLPGGRHLELRNIAVTSMSCDTPSFHPVPCVVDLSPINVSINF 731
DB 670 TYTTLQDGRTRRRLGFLPGGRHLELRNIAVTSMSCDTPSFHPVPCVVDLSPINVSINF 729
QY 732 SLMEEGTTPDQRAQKDIPIPLRSLHSETWIEPFKKNGCGDKCEANLTVSFPASRSR 791
DB 730 SLMEEGTTPDQRAQKDIPIPLRSLHSETWIEPFKKNGCGDKCEANLTVSFPASRSR 786
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QY 792 ALRLTAPASLSVELSLNTERDAYWQDLHFPFGSLSTRKYBMLKPHSQIPVSCHELPEE 851
DB 787 PLRLMSSASLAVENTLTSNGEDAYWVRDLDFPGLSRFKYEMLOPHSRMPVSCHELPEE 846
QY 852 SRLSLRALSNCVSSPIFAGHVALQWMTLVNWSMCDSEYELNANTVCNNEEDSLIEDN 911
DB 847 SSLRTKTKCNVSSPIFAGHVALQWMTLVNWSMCDSEYELNANTVCNNEEDSLIEDN 906
QY 912 SATTIPIPLYPINILIDQEDSTLYVSEPTPKGPIHGVKMYOVRIOPSIDHNIPTLEA 971
DB 907 SAATHPIPLYPINILITKEQENSTLYISFTPGPKTQVQVHYQVRIQSAVDHNPTEA 966
QY 972 VVGVPQPSSEPIRTHQSVQWQEPVPCYEDLER-LPDAAPCLPGLFPCPVVPROEIL 1030
DB 967 LVGVPQPSSEPIRTHQSVQWQEPVPCYEDLER-LPDAAPCLPGLFPCPVVPROEIL 1026
QY 1031 VQVIGTTELVEIEBASWFSICSSISIFSNSSKIFHLVGNASIAQVMAKYDVVYERQML 1090
DB 1027 IQVIGTTELVEIEBASWFSICSSISIFSNSSKIFHLVGNASIAQVMAKYDVVYERQML 1086
QY 1091 YLYVLSGIGLLLLLLPIVLVYKVPFKRNLIKERMAGRGVNGIPAEBSOLA-SQGEA 1149
DB 1087 HYYVLSGIGLLVLLPIVLVYKVPFKRNLIKERMAGRGVNGIPAEBSOLA-SQGEA 1146
QY 1150 GDPGCLKP 1157
DB 1147 KDMGCLBP 1154

RESULT 8
Q8HZV0 PRELIMINARY; PRT; 927 AA.
AC Q8HZV0;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Lymphocyte function-associated antigen 1 (fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Ovis; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Thumblak P., Kannan M.S., Maheswaran S.K.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AF440778; AAN63636.1; -.
DR HSBP; P20701; IDQO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0005515; P:protein binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF01839; FG-GAP; 2.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRIN.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS0234; VWF_A; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 927
SQ SEQUENCE 927 AA; 102522 MW; 02E2CF09917081BC CRC64;

Query Match
Best Local Similarity 59.7%; Score 3644.5; DB 2; Length 927;
Matches 706; Conservative 84; Mismatches 134; Indels 1; Gaps 1;
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QY 196 VQFSTSYKTEBDFSDYVVRKDPDALLKHVKHMLLTNTFGAINVAVTEVFEELGARDPA 255
D 4 VQFSTYRTEBTEFLDYIRKQDPDMLLAGVKHMLLTNTFGAINVAVKAVFPDLGARDPA 63
QY 256 TKVTLITTDGATDSGNIDAKDILRIYIIGIKHFOYKESQETLHKFASKPSEFVKILD 315
D 64 TKVTLITTDGATDSGNIDAKDILRIYIIGIKHFOYKESQETLHKFASKPSEFVKILD 123
QY 316 TFEKLDLFTLEOKKIYIEGTSKODLTSFMNELSSSGISADLSGHHVAVGAKDMAG 375
D 124 TFEKLDLFTLEOKKIYIEGTSKODLTSFMNELSSSGISADLSGHHVAVGAKDMAG 183
QY 376 GFLLDKADLQDDTFIGNEPITPEVAVAGLYGVTVLTPROKTSLLASGAPRYOHMGVTL 435
D 184 GFLLDKADLQDDTFIGNEPITPEVAVAGLYGVTVLTPROKTSLLASGAPRYOHMGVTL 243
QY 436 FOEPOGGHMSQVOTIHGTQIGSYFGGELCGVDVDQDETELLIGAPLYGEORGRVF 495
D 244 FOEPOGGHMSQVOTIHGTQIGSYFGGELCGVDVDQDETELLIGAPLYGEORGRVF 303
QY 496 IYOROLGFEVSELOSDGYPGRFGBATLTDINDGILVDVAVGAPLEEGAVVYFN 555
D 304 IYOROLGFEVSELOSDGYPGRFGBATLTDINDGILVDVAVGAPLEEGAVVYFN 363
QY 556 GRHGLSPQSPQRIEQTQVLSGIQWFGSIHGVNDLEBGDLADAVAGAESQMIYLSRPV 615
D 364 GQGGGLSPRSPQRIEQTQVLSGIQWFGSIHGVNDLEBGDLADAVAGAESQMIYLSRPV 423
QY 616 VDMYTLSPSPAPLPEVHEVCSYSTSNMKEGVNTTTPQIKSLYPOGRVANLYTL 675
D 424 VDMYTLSPSPAPLPEVHEVCSYSTSNMKEGVNTTTPQIKSLYPOGRVANLYTL 483
QY 676 QLDGRTERRRGLPFGGRHELRNIAVTSMGCTDPSFHPVCYODLSPINVSINFSIME 735
D 484 QLDGRTERRRGLPFGGRHELRNIAVTSMGCTDPSFHPVCYODLSPINVSINFSIME 543
QY 736 BEGTPRODROAKDIPILRPSLSETHWIEPEKNCGEKCEANLRYFSFASRALRT 795
D 544 BEGTPRODROAKDIPILRPSLSETHWIEPEKNCGEKCEANLRYFSFASRALRT 603
QY 796 TAPASLSEVLSLNEEDAVYVOLDLHPRPGLSPKRVEMLKHPSQIPVSCBEPBSRL 855
D 604 TAPASLSEVLSLNEEDAVYVOLDLHPRPGLSPKRVEMLKHPSQIPVSCBEPBSRL 663
QY 856 SRAISCNVSPPIFKAGHSVALOMMENTLVNSMGDSVSLHANNVCONNDSOLLBNATY 915
D 664 SRAISCNVSPPIFKAGHSVALOMMENTLVNSMGDSVSLHANNVCONNDSOLLBNATY 723
QY 916 IIPILYRINILIOQDESTLYVFTPKPKLHOVKMTQVRIOPSIHDMIPTLEAVGV 975
D 724 IIPILYRINILIOQDESTLYVFTPKPKLHOVKMTQVRIOPSIHDMIPTLEAVGV 782
QY 976 POPSESEITQMSVQVNEPRVPCYHEDLERLDDAERPLPACPCVAVFQOZILVOYIG 1035
D 783 POPSESEITQMSVQVNEPRVPCYHEDLERLDDAERPLPACPCVAVFQOZILVOYIG 842
QY 1036 TLELVEIASSMSLSSLSISFNSSKHFLXGNSLAQVMKVNDVVEKMLLYVL 1095
D 843 TLELVEIASSMSLSSLSISFNSSKHFLXGNSLAQVMKVNDVVEKMLLYVL 902
QY 1096 SGIIGLILILIFLYLVKVGFFKEN 1120
D 903 SGIIGLILILIFLYLVKVGFFKEN 927

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RESULT 9
Q6KAS4 PRELIMINARY; PRT, 1188 AA.
AC Q6KAS4
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

```

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DE MFLJ00114 protein (Fragment).
GN Name=MFLJ00114;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_taxonomy:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Kikuno R., Nakagawa T., Nagase T., Ohara O., Koga H.,
RT "Prediction of the Coding Sequences of Mouse Homologues of Flt Genes:
RT The Complete Nucleotide Sequences of 110 Mouse Flt-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries."
RL DNA Res. 11:167-180(2004).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the Integrin alpha chain family.
DR EMBL; AK131133; BAD21383.1; -.
DR HSPB; P17301; IAOX.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; TMS.
DR InterPro; IPR004043; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRIN.
DR PRINTS; PR04453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
DR PROSITE; PS50234; VWF_A; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON TER 1
SQ SEQUENCE 1188 AA; 131248 MW; BD93107BDB4178 CRC64;

Query Match 25.9%; Score 1583.5; DB 2; Length 1188;
Best Local Similarity 34.4%; Pred. No. 5,4e-95;
Matches 416; Conservative 213; Mismatches 467; Indels 115; Gaps 37;

QY 4 SCITVMAALLSGFFPAPASSYNDVRGARSPPRAGHPRGRTYQVNG-VIYAPG 62
D 21 SC-TWIAFLILLG---FVSCLGFLNDAEKPTNHR--MDGAFGHSVLYQYDSSWVVGAPK 74
QY 63 E--GNSTGLYOQOSGTGHCPLVTLR-GSNYTSKYLGMTLATDPTGSIACDPGRSRT 118
D 75 EIRATNIGELKYKCGHTGNCERPSISLOVPRPAVMSGLSLAATNPMSWLLACGPTVYHNT 134
QY 119 CDQNTYLSGLCYL---FRONTLOQPMLOGRPFQECIKANVDLVPLFDGSMISLOPBEFOK 174
D 135 CRENIYVLTCFLFLSSFGKQSNFPFAQ-----QECPKQODIVFLIDSGSISSTDPEK 189
QY 175 ILDPMDKVMKSLNSTSQPFAVQSPSTSYKTEPDPSPDVVRKDDALLKHVKHMLLTNTF 234
D 190 MLDPVKAVMQLOLRPSTRFSLMOPSDYRVHFTFNNEITSSPSLSDVSROLRGYTTA 249
QY 235 GAINVAVTEVFEELGARPATKVLITTDG-BATDSGNIDA-----ANDIIRYIIGIG 287
D 250 SAIRHVTLEFTTQSGARKQATKVLITTDGKQGDNLSDSYIPMAEASITIRYALGVG 309
QY 288 KHPQTKESQETLHKFASKPASEFVKILDTPEKLDLFTLEOKKIYIEGTSKODLTSFNM 347
D 310 KAFYNHKSQELKAIKMSPHSEYVSVENFDALKDIDNOKKIKI PAIEGTETPTSSSTFEL 369
QY 348 ELSSSGISADLSRKHAVVAVGAKDMAGGLDLKADLQDDTFIGNEPITPEVAVAGLYGV 407
D 370 EMSQEGFSAVFTDPDGLVAVGSPSWSGAFLYPSNMR-PTFINMGSEMDMDAYIGYS 428
QY 408 VTWLPSSQKTSLLASGAPRYOHMGVTLFOEPOGGHMSQVOTIHGTQIGSYFGGELCGV 467
D 429 -TALAFKGVHSLILGAPRQHTQKVIIF--TQBSRHRKPKSEVRGTQISYGAISLCSV 485
QY 468 DVDQDETELLIGAPLYGEORGRVFIYOROLG--FEEVSELOSDGYPGRFGBATL 525

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Db DMDRDSIDLVLIVGPHYHTRGQGVSCWPGVGRBMHCGTTLHGEGHPMGRFGAL 545
Qy 526 TALTDINGDLVAVGAPLEQ--GAYITENG-RHGCLSPQSPQRIETQVLSGIQMG 582
Db 546 TVLGVNDLADLAVAGAPGEEENGAAYIFHGAEROIAPSPORISASQIPSIQYFG 605
Qy 583 RSHGVKOLEGDLVAVGASOMIVSSRPVVMATLMSPPAIPVHEVGEYSUN 642
Db 606 QSLSGQDLTRDGLVAVGSKRVLLKRLPILSLVPTVHTPILSRVSVECEQVAP 665
Qy 643 KMKEGVNTTICPOIATLPVQFQGLVAVLTYTLQDGHTRRRGHPGGR-HELRRNIAY 701
Db 666 EGTLS-DATVCLIHESPTQGDRLSTVTPDLADHRLSTRALFKTKRALRVTVL 724
Qy 702 TTSNSCTDPSFHFVYCVODLSPINVSINFSIMEEGTPRDQAOCKDIPILRPSLSE 761
Db 725 GLNKHCESVKLLPACVEDSVPTILRLNFSL--VGVPISL--QNLQPLW--AVDQ 776
Qy 762 TW--EIPFKNCGDKXCEANLRSFSPARSRALRLAFASLVELSLNLEDAVWQ 818
Db 777 TLTASLPEKXCGADHICQDDLVSFVGFPPDLKTLVGSDELAVDVVNSDGEBSYGT 836
Qy 819 LDHPPGLSFKV--MLKPHSQ-----IPVCEELPEESRLSRALSCVNS 864
Db 837 VTLPFVGLSRRVABGVFLAKKEDQWQRGSHLMCDSTDRQGL-WSTSCSR 895
Qy 865 SPIFAGSHVALQWMENTLVNSWSDVELHANVTCNNEDSLLBNSATTI--IPILY 921
Db 896 HVIFFGSGMFLVFDVSPKAEGLDRLRLARVSENN--VGTPTFTQLPLVXY 951
Qy 922 PINILIQOEDSTLYVSF--TPKGPRIHQVKNYQVRIQPSIDHNIPL----- 969
Db 952 AVYTMISSHDQFTKLNFSSEKETSVEHNFVN--NLGQRPVPSINFWPIELKG 1008
Qy 970 EAVVGPVPPSEGPITTHOMSVOMEP--VPVCHYDLLELPAPAPCPGALFRCPVFR 1026
Db 1009 EAVVVMVNSHPQNPITOCRRNRKATQDFLTHQKSPVLDOSIADCLH--LRCD---- 1061
Qy 1027 QEILVQVIGTL-ELVGEIEASSMFS-----LCSSLSISFNSSKHPLVGSNSL 1074
Db 1062 ----IPSLGILDELFLIKGNLSFGMISQTLQKVLILSBAITFNTVSYSQGLPQBAFL 1117
Qy 1075 -AQVMKADVVEKMLVLYLSIGILLILITVLYKGFPRKMKKKKAEARG--V 1131
Db 1118 RAQTKTVEEMKVNHPVPLVIGSSVGGILLALITAILIKGFFRQYKEMLEBANQFV 1177
Qy 1132 PNGIPADESQ 1142
Db 1178 SDGTPPOVAQ 1188

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CC recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
CC interaction during inflammatory responses. It is especially
CC important in monocyte adhesion and chemotaxis (By similarity).
CC -1 SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
CC associates with beta-2 (By similarity).
CC -1 SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1 DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1 SIMILARITY: Belongs to the integrin alpha chain family.
CC -1 SIMILARITY: Contains 1 FG-GAP repeats.
CC -1 SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF211864; AAF23492.1; -.
CC HSSP: P20702; IN3Y.
CC MGD: MGI:96609; Itgax.
CC GO: GO:0009897; C:external side of plasma membrane; IDA.
CC InterPro: IPR000413; Integrin_alpha.
CC InterPro: IPR002035; VWF_A.
CC Pfam: PF01839; FG-GAP; 3.
CC Pfam: PF00357; Integrin_alpha; 1.
CC Pfam: PF00092; VWFA; 1.
CC PRINTS: PR01185; INTEGRINA.
CC PRINTS: PR00453; VWFADOMAIN.
CC SMART: SM00191; Int_alpha; 5.
CC SMART: SM00327; VWFA; 1.
CC PROSITE: PS00242; INTEGRIN_ALPHA; 1.
CC PROSITE: PS50234; VWFA; 1.
CC KX Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
CC Repeat; Signal; Transmembrane.
CC FT SIGNAL 1 19
CC FT CHAIN 20 1169
CC FT DOMAIN 20 1116
CC FT TRANSMEM 1117 1137
CC FT DOMAIN 1138 1169
CC FT REPEAT 34 87
CC FT REPEAT 88 ?
CC FT DOMAIN 152 330
CC FT REPEAT ? 402
CC FT REPEAT 403 454
CC FT REPEAT 456 518
CC FT REPEAT 519 577
CC FT REPEAT 582 634
CC FT CA_BIND 467 475
CC FT CA_BIND 531 539
CC FT CA_BIND 594 602
CC FT STB 1140 1144
CC FT DISULFID 69 76
CC FT DISULFID 108 126
CC FT DISULFID 656 711
CC FT DISULFID 770 776
CC FT DISULFID 858 873
CC FT DISULFID 1007 1031
CC FT DISULFID 1036 1041
CC FT CARBOHYD 89 89
CC FT CARBOHYD 267 267
CC FT CARBOHYD 393 393
CC FT CARBOHYD 734 734
CC FT CARBOHYD 949 949
CC FT CARBOHYD 1059 1059
CC FT CARBOHYD 1084 1084
CC SQ SEQUENCE 1169 AA; 129150 MW; C616412033C219A6 CRC64;

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Query Match 25.9%; Score 1582.5; DB 1; Length 1169;  
 Best Local Similarity 34.4%; Pred. No. 6,16-95;  
 Matches 416; Conservative 214; Mismatches 466; Indels 115; Gaps 37;



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Qy 4 SCITVMAALLSGFFFPASSYINLDVGRASSFPSPRAGRHYKVLQVANG-VIVGAPG 62
Db 2 SC-TWIAFLLLIG---FVSCIGFNLDAEKLTFFH--MDAGFGRHVLQYDSWVYVGA 55
Qy 63 E---GNSTGSLYOCOSGTHCLPVTLR-GSNYSKYLKMTLATPTDOSIACDGLSRT 118
Db 56 EIKATNOIGGLYKCGYHNTGCEPISLQVPPAVNLSISLAAATNPSMLACGPTVHT 115
Qy 119 CDONTYLSGLCYL-----FRONTQGPMLQGRPGFOECIGKGVNDLVLPFGSGMSLOPDEQX 174
Db 116 CREMTYLTGLCFLLSSSKOSONPTAQ-----QECFQODQIVFLIDSGSISSTDEK 170
Qy 175 ILDFMKDVKKLSTNSYQPAVQSTYKTEPDFSDYVKRDPDALLKHVHMLLTNTF 234
Db 171 MLDFFKAVMSQLOPSTPSTFSLMQFSDYFRVHFTFNFPSTSSPLSLSSVQLRGYVTA 230
Qy 235 GAINVVADEVREELGAPDPATKULITTDG-EATDSGNIDA-----AKDILRTITIG 287
Db 231 SAKHVITELFTTOSGARQADATKVLIVTDRKQGDNSYDSVLPMAASIIRYALIGV 290
Qy 288 KHPQTESQETLHKFASKPASEFVILDTPEKLDLFTLOKQIVIEGTSKQDLSPNM 347
Db 291 KAFVHESKQELKAIASMPSHYPSVNFALKDIEMLKREKIFALIGTETPSSSTEL 350
Qy 348 ELSSGSIADLSRGHAVVAVGAKDMAGFLDLKADLDDTFIENBPLTPEVRAGYLGYT 407
Db 351 EMSQEGFAVFTPDGPVLGAVGFSWGSAGFLYPSNMK-PPIFNNSGEMDRADYLGYS 409
Qy 408 VTMFPRSKTSLASGARFYQMGHVLFOEPQSGHNSQVOTIHGTQISYFGSELGV 467
Db 410 -TALAFMWGVHSLIGAPRHQHTGKVIF--TOBSRHRPKSEVAGTQIGSFFGSLCSV 466
Qy 468 DVDQDETLELLIGAPLFYGEORGGRVFIYQOROLG--FEEVSELQGPYGLRFGBAI 525
Db 467 DMDRQSDVLVIGFPHYHETHTRGQVSCPMFVGSGHMGCTILHGQGHMGRFGAL 526
Qy 526 TALVDINGDLVAVAGAPLEBO--GAVYIFNG-RHGGLSQPSQRIEGTOVLSGIQWFG 582
Db 527 TVLDGVNDGLADVAIGAEGEENRGAVYIFHGASRQDIAPSPQRIASQIPSLQYFG 586
Qy 583 RSHGVKDLBEGDLADVAVGASQMTVLSRPVDMVTLMSPFALIEVHEVCEGYSISN 642
Db 587 QSLSGGQDLTRDGLAVAGSGKRVLLRTRPILVSGPTVHTFPAEIRSVFCEQGVAP 646
Qy 643 KMKGVNTTICFOIKSLVPOFQGRLVANLTYLQDGRTRRGFPGR--HELRBNIAV 701
Db 647 EQILS-DATVCLIHESPKTQGLDKRSIVTFDLALDHGRSLTRALFKETKTRALTRVKT 705
Qy 702 TTSMSCDTPSFHFPVCVQDLISPIVNSLNFSLMEEGTPRDQRAQGDIPILRPSLSE 761
Db 706 GLNHGCEVKKLLPACVEDSVTPITLRNFSL---VGVPISL---QNLQFML--AVDDQ 757
Qy 762 TW---EIFEVOCCEDKKCEANLKVSEBPASRALRLTAFASLSVELSLNLEDAVWQ 818
Db 758 TYFASLPEFKNCGADHICQDDLSVFFPDLKTLVNSDLELNDVAVSHDGEBSYCTT 817
Qy 819 LDLRPPGLSPRYKE-----MLKPHSQ-----IPVSCBELPESRLLSRALSCVNS 864
Db 818 VTLVPVGLSPRRVAVEGVFLRKEDQOMQRGQSHLMDCSYDPRQGL-WSTSCSR 876
Qy 865 SPIFKAGHVALQWFMFTLVANSSWGDSEVELHANYTCNNEDSDLEDNAGATT---IPILY 921
Db 877 HVIFRGSGQMTFIVTFDVSPPKALIGDRLLRLARVSENN---VPGTKTTFQLELPKY 932
Qy 922 PINLIQOQEDSTLYVSF-TPKGKTIHOVKMYQVRIQPSIHDNIPFL-----969
Db 933 AVYTMISSHDQFTKTLNSTSEKETSVEHRFYVN---NLGQRDVPVSIINFVWIELKG 989
Qy 970 EAVVGVPPSPSEGLPTTHQWSQMEP---PVPCHVEDLERLDDAEPCLPGALFRPVPVFR 1026
Db 990 EAVVTWVSHQNPQLTQCYRNRRLKFTQPLDLTHQKSPVLQCSLADCLH---LRCD--- 1042

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Qy 1027 QEILVOVIGTL-ELVGEIEASNMFSS-----LCSSLSISFNSKHFHLYGNASL 1074
Db 1043 ----IPSLGILDELXYFIKGNLSFGWISQTLQKKVLLLSBAITFNYSVSQLFGQAF 1098
Qy 1075 -AQVVMVDVVEKQMLYLVVLSGIGLLLLIFLYLVKVPFKRLKXEMGRG--V 1131
Db 1099 RAQKRTVLEMYKXNPPVLLVGVSSVGLLLAILTALVYRAGFPKRYKMLERANQFV 1158
Qy 1132 PNGIARDSRQ 1142
Db 1159 SDGTPTPQVAD 1169

RESULT 11
ITAM HUMAN
ID ITAM HUMAN STANDARD; PRT; 1152 AA.
AC P1215;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor).
GN Name=ITGAM; Synonym=CD11b, CR3A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315033; PubMed=2457584;
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B."
RL J. Biol. Chem. 263:12403-12411(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88190151; PubMed=2833753;
RA Arnaout M.A., Remold-O'Donnell B., Pierce M.W., Harris P., Tenen D.G.;
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mo1: chromosomal localization and homology to the alpha subunits of Integrins."
RL Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257215; PubMed=2454931; DOI=10.1083/jcb.106.6.2153;
RA Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mo1 (complement receptor type 3).";
RL J. Cell Biol. 106:2153-2158(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93123748; PubMed=8419480;
RA Fleming J.C., Pahl H.U., Gonzalez D.A., Smith T.F., Tenen D.G.;
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution."
RL J. Immunol. 150:480-490(1993).
RN [5]
RP SEQUENCE OF 9-1153 FROM N.A.
RX MEDLINE=89098893; PubMed=2563162;
RA Hickey D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
RN [6]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=92073318; PubMed=1683702;
RA Shelley C.S., Arnaout M.A.;
RT "The promoter of the CD11b gene directs myeloid-specific and

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RT developmentally regulated expression.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).  
 RN [7]  
 RP SEQUENCE OF 1-9 FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=92144986; PubMed=1346576;  
 RA Paul H.L., Rosemarin A.G., Tenen D.G.;  
 RT "Characterization of the myeloid-specific CD11b promoter.";  
 RL Blood 79:865-870(1992).  
 RN [8]  
 RP SEQUENCE OF 17-31.  
 RX MEDLINE=87076671; PubMed=3539202; DOI=10.1016/0167-4838(86)90037-3;  
 RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;  
 RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation  
 across species and homology to platelet IIb/IIIa.";  
 RL Biochim. Biophys. Acta 874:368-371(1986).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-331.  
 RX MEDLINE=95171458; PubMed=7667070; DOI=10.1016/0092-8674(95)90517-0;  
 RA Lee J.O., Rieu P., Arnaout M.A., Liddington R.;  
 RT "Crystal structure of the A domain from the alpha subunit of integrin  
 CR3 (CD11b/CD18).";  
 RL Cell 80:631-638(1995).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.  
 RX MEDLINE=96363671; PubMed=8747460; DOI=10.1016/S0969-2126(01)00271-4;  
 RA Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;  
 RT "Two conformations of the integrin A-domain (I-domain): a pathway for  
 activation?";  
 RL Structure 3:1333-1340(1995).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.  
 RX MEDLINE=96363671; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;  
 RA Baldwin E.T., Sawyer R.W., Bryant G.L., Jr., Curry K.A.,  
 FA Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrichson R.L.,  
 RA Horton N.C., Kelley L.L., Milder A.M., Moon J.B., Mott J.E.,  
 RA Muchner V.T., Tomich C.S., Watempaugh K.D., Wiley V.H.;  
 RT "Calcium binding to the integrin CD11b I domain and activation model  
 assessment.";  
 RL Structure 6:923-935(1998).  
 RN [12]  
 RP 3D-STRUCTURE MODELING OF 17-616.  
 RX MEDLINE=96226734; PubMed=9560195; DOI=10.1073/pnas.95.9.4870;  
 RA Oxvig C., Springer T.A.;  
 RT "Experimental support for a beta-propeller domain in integrin alpha-  
 subunits and a calcium binding site on its lower surface.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).  
 CC -1- FUNCTION: Integrin alpha-M/beta-2 is implicated in various  
 adhesive interactions of monocytes, macrophages and granulocytes  
 as well as in mediating the uptake of complement-coated particles.  
 CC It is identical with CR-3, the receptor for the IgG fragment of  
 the third complement component. It probably recognizes the R-G-D  
 peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for  
 fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides  
 of fibrinogen gamma chain.  
 CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M  
 associates with beta-2.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in monocytes and  
 granulocytes.  
 CC -1- DOMAIN: The integrin I-domain (insert) is a VMPA domain. Integrins  
 with I-domains do not undergo protease cleavage.  
 CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
 CC -1- SIMILARITY: Contains 7 FG-GAP repeats.  
 CC -1- SIMILARITY: Contains 1 VMPA domain.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11b.htm".  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, J03925; AAA59544.1; -;  
 DR EMBL, M18044; AAA59491.1; -;  
 DR EMBL, J04145; AAA59903.1; -;  
 DR EMBL, S52227; AAB24821.1; -;  
 DR EMBL, S52152; AAB24821.1; JOINED.  
 DR EMBL, S52153; AAB24821.1; JOINED.  
 DR EMBL, S52154; AAB24821.1; JOINED.  
 DR EMBL, S52155; AAB24821.1; JOINED.  
 DR EMBL, S52157; AAB24821.1; JOINED.  
 DR EMBL, S52159; AAB24821.1; JOINED.  
 DR EMBL, S52161; AAB24821.1; JOINED.  
 DR EMBL, S52164; AAB24821.1; JOINED.  
 DR EMBL, S52165; AAB24821.1; JOINED.  
 DR EMBL, S52167; AAB24821.1; JOINED.  
 DR EMBL, S52169; AAB24821.1; JOINED.  
 DR EMBL, S52170; AAB24821.1; JOINED.  
 DR EMBL, S52173; AAB24821.1; JOINED.  
 DR EMBL, S52174; AAB24821.1; JOINED.  
 DR EMBL, S52180; AAB24821.1; JOINED.  
 DR EMBL, S52181; AAB24821.1; JOINED.  
 DR EMBL, S52184; AAB24821.1; JOINED.  
 DR EMBL, S52189; AAB24821.1; JOINED.  
 DR EMBL, S52191; AAB24821.1; JOINED.  
 DR EMBL, S52192; AAB24821.1; JOINED.  
 DR EMBL, S52203; AAB24821.1; JOINED.  
 DR EMBL, S52212; AAB24821.1; JOINED.  
 DR EMBL, S52213; AAB24821.1; JOINED.  
 DR EMBL, S52216; AAB24821.1; JOINED.  
 DR EMBL, S52219; AAB24821.1; JOINED.  
 DR EMBL, S52220; AAB24821.1; JOINED.  
 DR EMBL, S52221; AAB24821.1; JOINED.  
 DR EMBL, S52222; AAB24821.1; JOINED.  
 DR EMBL, S52226; AAB24821.1; JOINED.  
 DR EMBL, M76724; AAA58410.1; -;  
 DR EMBL, M84477; AAA51960.1; -;  
 DR PIR, A1108; RWH01B.  
 DR PDB, 1A8X; Model; @=17-1152.  
 DR PDB, 1BHO; X-ray; 1/2=-.  
 DR PDB, 1IDN; X-ray; 1/2=-.  
 DR PDB, 1IDO; X-ray; @=140-331.  
 DR PDB, 1JLM; X-ray; @=143-334.  
 DR PDB, 1MIU; X-ray; A=137-331.  
 DR PDB, 1MF7; X-ray; A=144-337.  
 DR PDB, 1N9Z; X-ray; A=140-335.  
 DR PDB, 1N45; X-ray; A=144-345.  
 DR Genew; HGNC:6149; ITGAM.  
 DR MIM, 120980; -;  
 DR GO; GO:0008305; C:integrin complex; TAS.  
 DR GO; GO:0007155; P:cell adhesion; TAS.  
 DR InterPro; IPR000413; Integrin\_alpha.  
 DR InterPro; IPR02035; VMP\_A.  
 DR Pfam; PF01839; FG-GAP; 3.  
 DR Pfam; PF00357; Integrin\_alpha; 1.  
 DR Pfam; PF00092; VWA; 1.  
 DR PRINTS; PRO1185; INTEGRINA.  
 DR PRINTS; PRO0453; VMPADOMAIN.  
 DR SMART; SM00191; Int\_alpha; 5.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
 DR PROSITE; PS50234; VMPA; 1.  
 DR 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;  
 KW Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 KM SIGNAL  
 FT CHAIN 1 16 Integrin alpha-M.  
 FT 17 1152  
 Query Match 25.6%; Score 1562.5; DB 1; Length 1152;  
 Best Local Similarity 34.3%; Pred. No. 1.2e-93;  
 Matches 408; Conservative 212; Mismatches 466; Indels 105; Gaps 37;

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Qy      6 ITWAMALLSGFFFPAPASSYNLDVGRARSPPRAGRHFGRVLYQV-GNGVIVAGAPE- 63
Db      6 LLLTALTLCHGF-----NLDTENAMTFQ--ENAGFGQSVYQLGSGVIVVAGAPEI 54
Qy      64 --GNGSTGSLVYCCSGTGCHLPVTLR-GSNYTSKYLGMTLADPDDGSLIADPGLSRCTCD 120
Db      55 VAAWQRSGSLVYCCDYSYSCBEPILRLQVPVEAVNMISLGLSLAATSPPLIACGPPVHQYCS 114
Qy      121 ONTYLSGLCYLFRONLQGPMLQGRPGFQECIKG-----NVDVLPFDGSMGSLQDPDEFOKIL 176
Db      115 ENTYVKGICLFLPGSNLR-----QDPQKPFELALRGCPQEDSDIAFLIDSGGSLIPDHFRMK 170
Qy      177 DPMKDVKKLSNTSYOFAAVOFTSYKTEFDFSDYVVKRKPDDALIKYKMHLLITNFGA 236
Db      171 EFVSTVMEQLKKSTLFLSLMGYSEFRHFFFKERQNNPNRSLVKEITQLGLGTHHTATG 230
Qy      237 INVYATVEFREELGARPDATVLLIITDGE--ATDSGNIDAKD-----ITRYIIIGIKH 289
Db      231 IRKVVRELFNITNGARKKAFKILVITDGEKFGDPLGEBDYIPEADREGVIRVYIGVDA 290
Qy      290 FQTESOETHKFPASKPASEFVKLIDPEKXKDLFTBLQKTYVEGTSKQDLSFNNEL 349
Db      291 FRSEKSKRELNTIASKPRPDHFOVNNFEALTKTIQNLREKIFALBEGYQSGSSSFEHEM 350
Qy      350 SSSGISADLSRGAHVAGAKDWAAGFLDKADLDQDTFIGNBPLTPEVRAGYLGYYVT 409
Db      351 SQBFSAITNGPLSTVSGYDWAAGVF-LYTSKEXKSTFINMTRVSDMNDATILGYAA 409
Qy      410 WLBRQKTSLLASGAPRYQHWGRVLLFQEPGCGHWSOVOTIHGTQIGSYGSELGYDV 469
Db      410 -ILIRNRVQSLVTDAPRYOHIGLVAMFR--ONTGMESNANAVKQIGAYGASISCSYDV 466
Qy      470 DQDETELLIGAPLFYEGORGRVFI--YGRROLGFEFVEBELQDDEPGYPLRGFEAITA 527
Db      467 DSKNSTDLVILGAHYHTEQTRGGQVSVPLRGRRKWCDAVLIGSQQPMGRGAALTV 526
Qy      528 LTTDINGDLVNAVAGAPLEE--QGAUYIFNGRHG-GLSPOPORIEGTQVLSGILQWFGRS 584
Db      527 LGDVNGDRLTVALGAPGEEDNRGAVVLFHGTSGSGISPSHSQRIAGSKLSPRLQYFQGS 586
Qy      585 IHGKYDLEGDLAVVAGAESQMLVLSRPVYDNTYLLSESPALIPVHEVCSYSTSKNM 644
Db      587 LSGQDILMDGLVLLTVGAGCHVLLLRQGPVLRVYALIMEFPRKARVAVFCNQV--KG 645
Qy      645 KEGVNITICFOI--SLVPOF--QGRLVANLTYTLQDGHRTRRGIFPGGRHELRNTAVT 702
Db      646 KEAGEVRVCLHVOXSTRDLRLEGOIQSVVITDLDLDSGRPHSRVFNETKSTRQTVL 705
Qy      703 -TSMCTDFSFHFVYVODLISPINVSINFLMEBEGTPRDQRAQGXKDIPIILRPSLHSE 761
Db      706 GLTGTCEMLKQLNCTIEDPVSPIVLRNLSL---VGRPLS--AFGN-----LAPVLAED 755
Qy      762 TWEL-----PEKXCGEDKCCBANLRVSPARSBALRLTLPASLSVELSLNTEBDAYW 816
Db      756 AQRFTLALFPKKKCGNDNICODDLSTIFSMISLCLVAGCPREPRNVTVVIRNGDEBSYR 815
Qy      817 VOJLHPPPGSLSPKRVEML---KPHSQIPVSCBELPERSRLLSRL---SCNVSSPIFKA 870
Db      816 TOVFFPPLDLSTYKRVSTLONQORSQWRKLACES--ASTEVSAKLSTGSSINHPIPE 873
Qy      871 GHSVALQMPNTLVNWSGDSVELEHANTYCNNEEDSLLEDNSATTI---IFILYPINILI 927
Db      874 NSEYFNITPVDKASLGKTLKANTSENN---MPRNKTBFOULELVKXAVVMV 929
Qy      928 QQDESDTLVYSFTEPKGIHQVKMYOYRIPSJHDHNIPTLEAVVGVPOPSGEPITHQ 987
Db      930 TSHSGSTKYLNFTASENSTRVMOHQYQV---SNLGOSLIP--ISLVFLVPAVLTQVIMDR 985
Qy      988 WSVQMEPPV--PCHYEDLERPDAAPECLPGLFRCPVY-----FRQ 1027
Db      986 PQTFFSENLSSTCHTK--ERLPSSHD--FLAELKRAPVNCSIAVCORIQCDIPFPGIQE 1041

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Qy      1028 EILVQVITGLIELVEGEIAS-SMFSLCSLSISFNSSKHFHLQYSNLSL-AQVWKKDVVY 1085
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Qy      1086 EKQMLYLYVYLSGIGLLILLIIFLYLYKVGFPFRNLKEREKAEARGVNGNP 1136
Db      1102 VNPFLPLVSSVGGILLLLIITAAVLYKGLGFFRQYKDMWSEG-GPGABP 1151

RESULT 12
ITAX HUMAN
ID ITAX HUMAN STANDARD; PRT; 1163 AA.
AC P20702; Q8IVA6;
DT 01-FEB-1991 (Rel. 17, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-X precursor (leukocyte adhesion glycoprotein p150, 95
  alpha chain) (leukocyte adhesion receptor p150, 95) (CD11c) (Lew M5).
GN Name=ITGAX; Synonyms=CD11c;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166645; PubMed=3327687;
RA Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
RT "cDNA cloning and complete primary structure of the alpha subunit of a
  leukocyte adhesion glycoprotein, p150, 95."
RL EMBO J. 6:4023-4028(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153906; PubMed=2303426;
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RT "Genomic structure of an integrin alpha subunit, the leukocyte p150, 95
  molecule."
RL J. Biol. Chem. 265:2782-2788(1990).
RN [3]
RP ERRATUM.
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RL J. Biol. Chem. 265:12750-12751(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
  Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
  Brownstein M.J., Udell T.B., Tsohyniki S., Carninci P., Prange C.,
  Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
  Fahey J., Helton B., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
  Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
  and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 20-43.
RX MEDLINE=87167596; PubMed=3549901;
RA Miller L.J., Wiebe M., Springer T.A.;
RT "Purification and alpha subunit N-terminal sequences of human Mac-1
  and p150, 95 leukocyte adhesion proteins."
RL J. Immunol. 158:2381-2383(1997).
CC -i- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It

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CC	recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell
CC	interaction during inflammatory responses. It is especially
CC	important in monocyte adhesion and chemotaxis.
CC	- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
CC	associates with beta-2.
CC	- SUBCELLULAR LOCATION: Type I membrane protein.
CC	- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC	granulocytes.
CC	- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC	with I-domains do not undergo protease cleavage.
CC	- SIMILARITY: Belongs to the integrin alpha chain family.
CC	- SIMILARITY: Contains 7 FG-GAP repeats.
CC	- SIMILARITY: Contains 1 VWFA domain.
CC	-1- DATABASE: NAME=PROV; NOTE=CD guide CD11c entry;
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd11c.htm".
CC	-----
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; M81695; AAA59180.1; -.
DR	EMBL; M29165; -; NOT ANNOTATED CDS.
DR	EMBL; M29487; AAA51620.1; ALT SEQ.
DR	EMBL; M29482; AAA51620.1; JOINED.
DR	EMBL; M29483; AAA51620.1; JOINED.
DR	EMBL; M29484; AAA51620.1; JOINED.
DR	EMBL; M29485; AAA51620.1; JOINED.
DR	EMBL; M29486; AAA51620.1; JOINED.
DR	EMBL; BC038237; AAH38237.1; -.
DR	PIR; A36584; RMHTIC.
DR	PDB; 1N3Y; X-ray; A=141-338.
DR	Genew; HGNC:6152; ITGAX.
DR	MIM; 151510; -.
DR	GO; GO:0008305; C:integrin complex; TAS.
DR	GO; GO:0004872; F:receptor activity; TAS.
DR	GO; GO:0007155; P:cell adhesion; TAS.
DR	GO; GO:0009887; P:organogenesis; TAS.
DR	InterPro; IPR000413; Integrin_alpha.
DR	InterPro; IPR002035; VWF_A.
DR	Pfam; PF01839; FG-GAP; 3.
DR	Pfam; PF00357; Integrin_alpha; 1.
DR	Pfam; PF00092; VWF_A; 1.
DR	PRINTS; PRO1185; INTEGRINA.
DR	PRINTS; PRO0453; VWFADOMAIN.
DR	SMART; SM00191; Int_alpha; 5.
DR	SMART; SM00327; VWF; 1.
DR	PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR	PROSITE; PS50234; VWFA; 1.
KW	3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
KW	Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
KW	Signal; Transmembrane.
KW	SIGNAL.
FT	CHAIN. 20 1163 Integrin alpha-X.
FT	DOMAIN. 20 1107 Extracellular (Potential).
FT	TRANSMEM. 1108 1128 Potential.
FT	DOMAIN. 1129 1163 Cytoplasmic (Potential).
FT	REPEAT. 34 87 FG-GAP 1.
FT	REPEAT. 88 ? FG-GAP 2.
FT	DOMAIN. 165 351 VWFA.
FT	REPEAT. ? 401 FG-GAP 3.
FT	REPEAT. 402 453 FG-GAP 4.
FT	REPEAT. 455 517 FG-GAP 5.
FT	REPEAT. 518 576 FG-GAP 6.
FT	REPEAT. 581 633 FG-GAP 7.
FT	CA_BIND. 466 474 potential.
FT	CA_BIND. 466 538 potential.
FT	CA_BIND. 593 601 potential.
FT	SITE. 1131 1135 GFPR motif.
FT	DISULFID. 69 76 By similarity.

Query Match	Similarity	Score	DB	Length
Beet Local	25.0%	1526.5	1	1163
Matches	421	Conservative	193	Mismatches 473; Indels 115; Gaps 40
12	ALLSGFFPFAASSNYLDVRGARSFSPRARHFGYVLQVNGG-VIVGARG--GNST	67		
6	AAALLFTLALSLSGNLDTEBELTAFRVDSAG--FQDSVVQVANSWVVGARQKITAANQT	63		
68	GSLYOCGSGTGHCLPVTLR-GSNVTSKYLGMTLATDPDSDSIACDPGLSFTCDONTYLS	126		
64	GLYOCGYSTACBCEPIGLQVPEAVNMSLGLSLSTSPSOLLACGPTVNHRCGNMYLT	123		
127	GLCYLFRNLQGP--MLQGRP-GROECIKGVNDLVPLFDGMSLSLOPDEFQKILDPMDVM	183		
124	GLCYFL-----GPYQLTQRLFVSRQECRQODIVFLDSDGSISSRNFAITMMFVRAVI	178		
184	KKLSTSYQFAVQFSTSYSTKTEPFDSDYVVKRQDPAALIKHGMILLTNTFGAINVYATE	243		

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Db 179 S Q F O R P S T Q S I M O F S N K F O T H F T F E E B R R T S N P L S L A S V H O L G F T Y T A T A I O N V H R 238
Qy 244 V E R B E I G A R P A T K V L I I T D - - - - G E A T D S G N I - - - - D A A K D I R Y I I G I G K P Q T K E S 295
Db 239 L F H A S Y G A R R A T K I L I V T T D K E G D S L D Y K D V I P M A D A - G I I R I A I G L A F O N E N S 297
Qy 296 Q E T I H K F A S K A S E F V K I L D T F E K K D F T E L O K K I Y I E G T S K O D L S F M M E L S S G I S 355
Db 298 W K E I N D I A S K P S O E H I F V E D P D A L K I O N Q L K E K I P A I E G H E T T S S S F E L E M A Q E F S 357
Qy 356 A D L S R G A V A N G A K M A G E F L D K A D L O D D T F I G N E P L P E V A G I L T T V T M L B R Q 415
Db 358 A V F P D G F V L A V G S F T W S G A F - L Y P P N M S P T F I M S O E N V D M K D S I L G Y S - T E L A L M K 415
Qy 416 K T S L I A S G A P R Y O H N G R V L F O E P O G G G H W S O V T I H G T O I G S Y G E G E L C G V D V D Q D E T 475
Db 416 G V O S I V L G A P R Y O H T K A V I F - T O V S R O M K M K A E V T O T O I G S Y G A S L C S V D V D T D S T 473
Qy 476 E L L I I G A D L F Y G E O R G R V F I Y Q R - - - - R O L G F E E V S E L Q D P G V P L G R F G A T A T A L D I 531
Db 474 D V I L I G A P H Y E Q R T G G Q V S C P L P R G M R M W C D A V - L Y G B Q G H P M G R F G A L T V L G D V 531
Qy 532 N G D G I V D A V A G A P L E E Q - - G A V Y I P N G H G - G L S P O P O R I E G T O V L S G I Q M F G S I T G V 588
Db 532 N G D K I T D V I A P G E E N R G A V I L F H G V L G P S I S P S H Q R I A G S Q L S R L Q Y F G O A L S G G 591
Qy 589 K O L E G D G L A D V A G A S Q M I V L S R P V D M T L M S F S P A E I P V H E V E C S Y S T S N K M K E G V 648
Db 592 Q D L O D G L A D V A G A R G O V L I R T P V L M G V S M O F I A E I P R K A F E C R E Q V A S E - Q T L V 650
Qy 649 N I T T C F O I K S I Y P O F Q R - - I V A N L T Y T L Q D G H R T R R R G L F P G G R H - E L R R N I A V T T S M 705
Db 651 Q S N I C L Y I D K S K N L G S R D L Q S S V T L D L A D P G L S P R A T Q E T K N R S L S V R V I G L K A 710
Qy 706 S C T D S S F R P V C V O D L I S P I N V S L A F S I M E E B G T R D R O A Q K D I P P I - L R P S I H S R - 761
Db 711 H C E N N L L P S C V E S E V P I T L R L N F T L - - - - - V G K P L A F R N I R P M L A A D Q 758
Qy 762 - - - T W E I P E R K N C G E D K C E A N L R V S F S P A N S R A L R L A P A S L S V E L S I N L E E B A V W Q 818
Db 759 R Y F T A S L P E R K N C G A D H I C O D N L G I S F S P G L K S L I V G S N L E L N A V M W M D G E D S Y G T T 818
Qy 819 L D L A P P P L S F R K Y E M L K P H S Q - - - I P V S C E L P E S R L S R A L S C N V S P I F K A G H S V A 875
Db 819 I T F S H P A G L S Y R V A E G Q K O G L R E I L H L T C S A P V G S Q - G T W S T S C R I N H I I F R G A Q I T 877
Qy 876 L O M E N T I V N S S K G S V E L H A N V T C N N E D S D L E D N S A T T I - - I P I L Y P I N I L I Q D O E D 932
Db 878 F L A A T F D V S P K A V L G D R L L L T A N V S E E N - - - T P R T S K I T T P O L E L P V K Y A V T V V S S H E Q 933
Qy 933 S T L Y V S F T P K G P K - I H O V G H Y O V A I O P S I H D H N I P T - - - - - L E A V V G V 975
Db 934 F T K I A N F E S E B E K E S H V A M H R Y Q V A - - - N L G O R D L P V S I N F V P V E L N O E A V M D V E V S H 990
Qy 976 P O P S E G B I T H O M S V O M E P V P C H E D E D E R L P D A E P C L P G A L - F R C P V - - - V F R O E I L V 1031
Db 991 P O N F S - - - - L R C S S E K I A P P A S D F L A H I Q K N P - V L D C S I A G L A R R C D V P S P S V G E I D F 1045
Qy 1032 Q V I G T L E L - - V E I A S S M F S I C S L S I S F N S S K F H L Y G S A S L A Q V M K D V Y E E Q M 1089
Db 1046 T L K E N L S G W A R O I - L O K K V S V A E I T F D T S V S O L P G C A F A R - - - A Q T T V L E K Y K 1101
Qy 1090 L Y - - - - L V V L S G I G L L L L L I F I Y L Y V Y G F P K R L K E M M E A R G - - - V P N G - I P A D S 1140
Db 1102 V A N P P L L V G S S I G G L L L A L I T A V L Y V G F P K R O K E M E B A N G O I A P E N G T O T P S P S 1161
Qy 1141 E Q 1142
Db 1162 E K 1163

```

RESULT 13  
ITAD\_RAT

```

ID ITAD_RAT STANDARD; PRT; 1161 AA.
AC O90Y7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor.
GN Name=Itgad;
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA O'Brien M.M., VanderVlieten M., Kilgannon P.D., Dietech G.,
RA Gallatin W.M.;
RT "Cloning of rat alpha D, a novel beta 2 integrin.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC from the blood (By similarity).
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
CC associates with beta-2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AF021334; AAF21241.1; -.
DR HSSP; P1215; 1BHQ.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWF; 1.
DR PRINTS; PRO0185; INTEGRIN.
DR PRINTS; PRO0453; VWFADOMAIN.
DR SMART; SM00337; VWF; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 1161
FT DOMAIN 1101 1121
FT TRANSMEM 1122 1161
FT DOMAIN 34 87
FT REPEAT 88 87
FT REPEAT 88 7
FT DOMAIN 152 334
FT REPEAT 352 402
FT REPEAT 403 454
FT REPEAT 456 517
FT REPEAT 519 577
FT REPEAT 582 634
FT CA_BIND 467 475
FT CA_BIND 531 539
FT CA_BIND 594 602
FT SITE 1126 1130
FT DISULFID 69 76

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FT DISULFID 108 126 By similarity.
FT DISULFID 656 711 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 845 860 By similarity.
FT DISULFID 993 1017 By similarity.
FT DISULFID 1022 1027 By similarity.
FT CARBOHYD 61 61 N-linked (GlcNAc...) (potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (potential).
FT CARBOHYD 393 393 N-linked (GlcNAc...) (potential).
FT CARBOHYD 696 696 N-linked (GlcNAc...) (potential).
FT CARBOHYD 734 734 N-linked (GlcNAc...) (potential).
FT CARBOHYD 784 784 N-linked (GlcNAc...) (potential).
FT CARBOHYD 907 907 N-linked (GlcNAc...) (potential).
FT CARBOHYD 936 936 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1045 1045 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 1161 AA; 126600 MW; 2258491A984705E CRC64;

Query Match 24.8%; Score 1516; DB 1; Length 1161;
Best Local Similarity 33.2%; Pred. No. 1.5e-90;
Matches 404; Conservative 207; Mismatches 465; Indels 142; Gaps 40;

13 LLSGFFPAASSYNDVAGASSFPSPRGRHGYRVLVQVNG-VVIGAPGEG--NSTG 68
8 LLDG-WVLASCHGSNLDVEEPIYFREDAS--FGQTVVQFGGSRVVGAPLEAVANNQ 64
69 SLVYOCSTGHCLEPTVLKGS-NYSKYLCMTLATDPTDGSIIACDGLSRTCDQNTYLSG 127
65 RLYDCAPATGMCQPIYLRSPLEAVNMSLGSLVATATNNAQLACGPTQACVKNMYAKG 124
128 LCVLPFRONIGPMLOGR-GFOECIKGVNDVFLPDSMSLOPDERQKILDMFMKMKL 186
125 SCLLAGSSIQ--PIQVVPASMPCEPQEMDIAFLIDSGSINORDAKMDPKALMGF 182
187 SNTSYQFAVQFSTSYKTEFSDYVKRQDPALLKRVKMLITTFPAINYVAIVER 246
183 ASTSTLSLMQYSNILKHTFTFERKNIIDPOSVDPIYQGLTITAGITWELFH 242
247 EERKARPDATKVLIIITDG---EATDSNIDAKD--IIRYIIGRHPOTKSOETL 299
243 SKRGSRKSAKILVITTDQKRDPLEYSDVIPAADKAGIIRAIQVGAQEPALKE 302
300 HKPASKPASEPVKILDTFEKMDLFELOKTIYVEGSKQDLTSNMELSSSGISADS 359
303 NTGSAPODHPFKVGNFALRSIQRLQEKI PALEGTSSRSSSQHMSQEGSSALT 362
360 RGHAVVGAAGAKOMAGFLDLKADLDODDFIGNEPLTPVRAGYLGYT--WLPSPROK 416
363 SDPVLGAVGFSWSGAF-LYPRNTRPTFIMSGENVMDRSYLGSTAVAFW----KG 417
417 TSULASGARVYOMGRVLLFOBPQGGHWSQVQTHGTQIGSYFGELCGVDVDDGETE 476
418 VNSLIGARRHQHTGVIF--TQEARHMRPKSEVAGTQIGSYFGSLCSVDVDRGSD 475
477 LLLIGAPLYEGEGRGRVITYQ---RRQLGFEVSELOGDPGPIGRGGAITALTIN 532
476 LVLLIGAPHYEQTRGGQVSVFPVPGVRGMOCE--ATLHGBOGHGPRGVALITYLDVN 533
533 GGLGVAVAGAPLEEO--GAVYIFNGRHG-GISPOSGRIEGQVLSGIOMFGRSIGHV 589
534 GMLADVALIGAGEEBSRGAVIIFRQASLETMPSSQVTSQSLRLQITFGQSLSGQ 593
590 DLBGDLADVAGASQOMIVLSSRPVDMVTLMSPAPRIPVHEVCSYSTSNKKEGVN 649
594 DLTQDGLVLAAGAQAQHVLRLSLPLKVELSIRFAPMEVAKAVYQCMWERTFVLEAG-E 652
650 IITPCIKSLVYQFQGRVANLTYTLQLDGHRTRRRGLFRGGRHERRIAIATTSMS--- 706
653 ATVCLLVHKGSPDLGNVGSVRYDIALPGRIRISAFI----DETAKCTTLGRKTLGL 707
707 ---CTDPSEHFPCVODLSPINVSINFLMEBEGPPROQAGKQIPIRLPSLSH--T 762
708 GHCEIVKLLLPDCVDAVSPITLRNLFVLVDSAPR-----NLHVLAVGSDHIT 760

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QY 763 WEIPKQCGEDKCKGEANLWVSPSPARALRLTAPASLYELSLSNLEADAYWQLDLH 822
DQ 761 ASLPKCKQCKGLCEGDLGISFNFSGLQVLVGGSPETITVTVWNGEDSYGLTVFY 820
QY 823 PPPGLSPFRKVKMLKPHSQIP--VSCCELPEESRLRLALSCVNSPIFKASHVALQWVF 880
DQ 821 YPAGLSYRVTCTOQPHQPLRLACEAPPAQEDL-RSSSCSINPIFRBAGKTFMTTF 879
DQ 881 NTLVNSWSDSVYELHANTCNNEEDLLEDSATTI-IPILYPINILIQDQDSTLYVSF 939
DQ 880 DVSVAFLGDRLLRLAKKASSENNKED--TNKTAFLQELPEVKTYYTLISRGDSYTHVNF 937
QY 940 TPK-GRKHQVQWVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 981
DQ 938 SSSHGRRQEAHARRV-----NLSPLKAVRVVFWVVLNGVAVMDVLTSSPAQ 989
QY 982 GPITHQMSVQMPVY-PCYEDLER--LPDAEBCPLGALPCPVVFRQETLVQVIGTL 1037
DQ 990 GV---SCVSQMKFPQNPDLFQIQRRSVLDCSIADCLH---FRCD-----ISL 1032
QY 1038 ELVGEIE-----ASSMFSLCSLSLISFNSKHFHLYGNSASI-AQVYMKV 1081
DQ 1033 DIQDELDFLRGNLSFGWVSQTLQEKVLLVSAEITPDTSVYSQLPQGEAFLAQVETTL 1092
QY 1082 D--VYEEKQMLTYLVLSIGILLLLLFYLYKYGKFRKNIKEMEGRGVPGNIPAD 1139
DQ 1093 BEYVYER--IFLVGSSVGGILLALITVLYLKGFPRKQYKEMLD-----GRA 1140
QY 1140 SEQLASQGEAGDPCGLK 1157
DQ 1141 ADPVTAQO--ADPGCETP 1156

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RESULT 14
ID ITAM MOUSE STANDARD; PRT: 1153 AA.
AC P05555; O8CA73;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
GN Name:Itgam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=88312584; PubMed=3044779;
RA Pyela R.;
RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor";
RL EMBO J. 7:1371-1378(1988).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S., Nukado I., Oeato N., Saito R., Suzuki H., Yamamoto H., Kiyosawa H., Yagi K., Tomaru Y., Haesgawa Y., Nogami A., Schenbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schiml L.M., Kanapin A., Matsuda H., Batilov S., Beisel K.W., Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustingich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Kongaya A., Kurochkin I.V., Lee Y., Lehman B., Lyons P.A., Maglott D.R., Maitais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,

```

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Vitorato R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carriotti P., Hayatsu N.,  
RA Hironaka-Kishikawa T., Komio H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Iehli Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
[3]  
RN SEQUENCE OF 11-45 FROM N.A.  
RP STRAIN=BALB/c; TISSUE=Spleen;  
RC MEDLINE=86287312; PubMed=2942940;  
RX Sastre L., Roman J.M., Teplov D.B., Dreyer W.J., Gee C.E.,  
RA Larson R.S., Roberts T.M., Springer T.A.;  
RT "A partial genomic DNA clone for the alpha subunit of the mouse  
RT complement receptor type 3 and cellular adhesion molecule Mac-1,"  
RL Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).  
[4]  
RN SEQUENCE OF 17-28.  
RP MEDLINE=85188276; PubMed=3887182;  
RX Springer T.A., Teplov D.B., Dreyer W.J.;  
RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion  
RT glycoproteins and unexpected relation to leukocyte interferon,"  
RL Nature 314:540-542(1985).  
CC -1- FUNCTION! Integrin alpha-M/beta-2 is implicated in various  
CC adhesive interactions of monocytes, macrophages and granulocytes  
CC as well as in mediating the uptake of complement-coated particles.  
CC It is identical with CR-3, the receptor for the ICB fragment of  
CC the third complement component. It probably recognizes the R-G-D  
CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for  
CC fibrinogen, factor X and ICAM-1. It recognizes p1 and p2 peptides  
CC of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in  
CC mast cell development and in immune complex-mediated  
CC glomerulonephritis. Mice expressing a null mutation of the alpha-M  
CC subunit gene demonstrate increase in neutrophil accumulation, in  
CC response to a impaired degranulation and phagocytosis, events that  
CC apparently accelerate apoptosis in neutrophils. These mice develop  
CC obesity.  
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M  
CC associates with beta-2.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=p05555-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=p05555-2; Sequence=VSP\_010473;  
CC Note=No experimental confirmation available!  
CC -1- TISSUE SPECIFICITY: Predominantly expressed in monocytes and  
CC granulocytes.  
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins  
CC with I-domains do not undergo protease cleavage.  
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.  
CC -1- SIMILARITY: Contains 1 VWFA domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X07640; CAA30479.1; -.

DR EMBL; AK039444; BAC30350.1; -.  
DR EMBL; M14293; AAA39484.1; -.  
DR PIR; S00551; S00551.  
DR HSSP; P11215; 1BHO.  
DR MED; MG196607; ItgAm.  
DR GO; GO:0009897; C:external side of plasma membrane; IDA.  
DR GO; GO:0007155; P:cell adhesion; IMP.  
DR GO; GO:0045123; P:cellular extravasation; IMP.  
DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.  
DR InterPro; IPR000413; Integrin\_alpha.  
DR InterPro; IPR020351; VWF\_A.  
DR Pfam; PF01839; FG-GAP; 3.  
DR Pfam; PF00357; Integrin\_alpha; 1.  
DR Pfam; PF00092; VWA; 1.  
DR PRINTS; PR01185; INTEGRINA.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR SMART; SM00191; Itc\_alpha; 5.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
DR PROSITE; PS50234; VWF\_A; 1.  
KW Alternative splicing; Calcium; Cell adhesion;  
KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;  
KW Signal; Transmembrane.  
FT SIGNAL 1 16  
FT CHAIN 17 1153  
FT DOMAIN 17 1105  
FT TRANSMEM 1106 1129  
FT DOMAIN 1130 1153  
FT REPEAT 31 84  
FT REPEAT 85 163  
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FT DOMAIN 337 400  
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Query March 24.88; Score 1514.5; DB 1; Length 1153;  
Best Local Similarity 33.88; Pred. No. 1.8e-99;  
Matches 407; Conservative 188; Mismatches 481; Indels 129; Gaps 36;  
QY 6 ITWAMALLSGFFAPASSYNLDVRCARSPPRAGRHFGYVLYQV-GNGVIWGAPEG 64



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Qy 307 ASEFYKILDTREKLDLFTLELOKIIYIEGTSKODLTSFNNMELSSSGISADLSRGHAAVG 366
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Qy 367 AVGAKDMAGG-FLDIKADLODDTFI GNEPLTPEVRAGYLTWTWLPBROKTSLLASGAP 425
Db 368 SVGSFDMAGAFLYPSKD--KASFINTRIDSDMNDAYIGYASAVI--SRNRVQSLVILGAP 424
Qy 426 RYOHNGRVTLFOEPQGGHWSQVOTIGHTOIGSYFGSELGVDVDQDGETELLIGAPLF 485
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Qy 486 YGBORGGHVF--YORROLGFEVSELOQDPGYLGRFGBAITALTIDINGDLVDVAVGA 543
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Qy 544 P--LEBQAVYTFNGRH--GGLSPQPSQRIEGTQVLSIGIOMFGRSIHGVYDLBGDGLADVA 600
Db 543 FGEOMOGAVYIFHGASVASISTPHSQRIAGARFSPGQYFGQSLSGGKDLTMDGLMDLA 602
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Qy 889 GDSVEILANVTCNNEEDSLLEDNSATTTIIPILYPINIILIOOEDSTLYVSTPKGPKIHQ 948
Db 891 GNKLILKVVVTSENNVS--RTDKTESQLELPVYAIYMWVTSGESIKEYIANFTASEMTSKV 949
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Search completed: August 29, 2005, 19:23:48  
 Job time : 121 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 29, 2005, 19:19:14 ; Search time 178 Seconds  
(without alignments)  
2582.717 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106  
Sequence: 1 MKDCSITMAMALLSGFFPFF.....DRCIKPLHKDSESGGKD 1170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	6106	100.0	1170	9	US-09-945-265-2
2	6106	100.0	1170	16	US-10-473-127-1743
3	6098	99.9	1170	15	US-10-261-164-1
4	6098	99.9	1170	16	US-10-473-127-1737
5	6098	99.9	1170	16	US-10-473-127-1737
6	6098	99.9	1170	16	US-10-473-127-1742
7	6098	99.9	1170	17	US-10-741-600-1088
8	6098	99.9	1170	20	US-11-062-290-1
9	6061.5	99.3	1223	17	US-10-741-600-1086
10	6053.5	99.1	1223	16	US-10-408-765A-295
11	6053.5	99.1	1223	16	US-10-473-127-1736

12	5981	98.0	1145	17	US-10-872-198-130	Sequence 130, App
13	5981	98.0	1145	20	US-11-021-951-130	Sequence 130, App
14	5973	97.8	1145	16	US-10-473-127-1738	Sequence 1738, App
15	5649.5	92.5	1086	16	US-10-473-127-1741	Sequence 1741, App
16	5585	91.5	1086	16	US-10-408-765A-1871	Sequence 1871, App
17	5585	91.5	1086	16	US-10-473-127-1735	Sequence 1735, App
18	5585	91.5	1086	16	US-10-473-127-1744	Sequence 1744, App
19	5585	91.5	1086	17	US-10-741-600-1087	Sequence 1087, App
20	5533.5	90.6	1065	16	US-10-473-127-1740	Sequence 1740, App
21	3066	50.2	589	15	US-10-261-164-2	Sequence 2, Appl1
22	3066	50.2	589	20	US-11-062-290-2	Sequence 2, Appl1
23	1563	25.6	1153	9	US-09-350-259-3	Sequence 3, Appl1
24	1563	25.6	1153	10	US-09-902-481A-1	Sequence 1, Appl1
25	1563	25.6	1153	10	US-09-891-943-3	Sequence 3, Appl1
26	1563	25.6	1153	14	US-10-144-259-30	Sequence 30, Appl1
27	1563	25.6	1153	14	US-10-207-655-176	Sequence 176, App
28	1562.5	25.6	1152	9	US-09-945-265-4	Sequence 4, Appl1
29	1557.5	25.5	1137	10	US-09-902-481A-5	Sequence 5, Appl1
30	1552.5	25.4	1137	10	US-09-902-481A-6	Sequence 6, Appl1
31	1547.5	25.3	1137	10	US-09-902-481A-4	Sequence 4, Appl1
32	1536.5	25.2	1137	10	US-09-902-481A-3	Sequence 3, Appl1
33	1521.5	24.9	1163	15	US-10-116-275-204	Sequence 204, App
34	1521.5	24.9	1163	16	US-10-723-660-127	Sequence 327, App
35	1515.5	24.8	1163	18	US-10-794-899-100	Sequence 100, App
36	1504	24.6	1161	9	US-09-350-259-55	Sequence 55, Appl1
37	1504	24.6	1161	10	US-09-891-943-55	Sequence 53, Appl1
38	1490	24.4	1161	9	US-09-350-259-53	Sequence 53, Appl1
39	1490	24.4	1161	10	US-09-891-943-53	Sequence 4, Appl1
40	1480.5	24.2	1163	10	US-09-350-259-4	Sequence 4, Appl1
41	1480.5	24.2	1163	10	US-09-891-943-4	Sequence 2, Appl1
42	1476	24.2	1161	9	US-09-350-259-2	Sequence 2, Appl1
43	1476	24.2	1161	10	US-09-891-943-2	Sequence 2, Appl1
44	1475.5	24.2	1161	9	US-09-350-259-99	Sequence 99, Appl1
45	1475.5	24.2	1161	10	US-09-891-943-99	Sequence 99, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-945-265-2  
Sequence 2, Application US/09945265  
Patent No. US20020123614A1  
GENERAL INFORMATION:  
APPLICANT: Springer, Timothy A.  
APPLICANT: Shimaoka, Motomu  
APPLICANT: Lu, Chafen  
TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A  
FILE REFERENCE: CEN-002CP  
CURRENT APPLICATION NUMBER: US/09/945,265  
CURRENT FILING DATE: 2001-08-31  
PRIORITY FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: US 60/229,700  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-945-265-2

Query Match 100.0%; Score 6106; DB 9; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MKDCSITMAMALLSGFFPFPASSYNDVAGASFSPPRGRFRGVLOVNGVYGA 60  
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; Sequence 1743, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1743  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1743

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Best Local Similarity 100.0%; Pred. No. 0;  
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Qy      601 VGASEQMTVLSRRPVVDWMTLMSSEPAIIPVHEVCSTSTSNKMEGVNITICFOIKSLY 660
Db      601 VGASEQMTVLSRRPVVDWMTLMSSEPAIIPVHEVCSTSTSNKMEGVNITICFOIKSLY 660
Qy      661 POFQGRIVANITVTLQLDGHRTRRGLPPGGHRLRNIAVTTSMSCDTFSFHPVCQD 720
Db      661 POFQGRIVANITVTLQLDGHRTRRGLPPGGHRLRNIAVTTSMSCDTFSFHPVCQD 720
Qy      721 LISPIVSLNFSLMBEETPRDQAOQKDIPIILPRLSHSTWEIIPFEKNGCEDKCCAN 780
Db      721 LISPIVSLNFSLMBEETPRDQAOQKDIPIILPRLSHSTWEIIPFEKNGCEDKCCAN 780
Qy      781 LRVSPSPARSRLRLTAFASLSVELSLNLEEDAVWQDLHPFGLSFRKYEMLKPHSQ 840
Db      781 LRVSPSPARSRLRLTAFASLSVELSLNLEEDAVWQDLHPFGLSFRKYEMLKPHSQ 840
Qy      841 IPVSCBELPEBSRLSLRSLSCNVSSPIFKAGSHVALQMMFNTLVNNSWGSDELHANTC 900
Db      841 IPVSCBELPEBSRLSLRSLSCNVSSPIFKAGSHVALQMMFNTLVNNSWGSDELHANTC 900
Qy      901 NNEDSDLEEDNSATITIPILYPINILIQOEDSTLYVSTFKPKGIHQVKMYQVRIOPS 960
Db      901 NNEDSDLEEDNSATITIPILYPINILIQOEDSTLYVSTFKPKGIHQVKMYQVRIOPS 960
Qy      961 IHDNIPITLBAVVGVPQPSSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGALFR 1020
Db      961 IHDNIPITLBAVVGVPQPSSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGALFR 1020
Qy      1021 CPVVRQELIVQVITGLTLEVGELIEMSMFSLCSSLSTISFNSSKHHLVGSNASLAQVVMK 1080
Db      1021 CPVVRQELIVQVITGLTLEVGELIEMSMFSLCSSLSTISFNSSKHHLVGSNASLAQVVMK 1080
Qy      1081 VDVIYKEMQMLYLYVLSIGILLLLIFIVLYKVGFFRKNLKEKMEAGRGVNGI PAEDS 1140
Db      1081 VDVIYKEMQMLYLYVLSIGILLLLIFIVLYKVGFFRKNLKEKMEAGRGVNGI PAEDS 1140
Qy      1141 EQLASGEADGPGCLKPLHEKDSSEGGKD 1170
Db      1141 EQLASGEADGPGCLKPLHEKDSSEGGKD 1170

RESULT 3
US-10-261-164-1
; Sequence 1, Application US/10261164
; Publication No. US20040062765A1
; GENERAL INFORMATION:
; APPLICANT: KAPUSTAY, PAMELA M.
; APPLICANT: LEWIS, REX H.
; TITLE OF INVENTION: LPA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: 046007/0272304
; CURRENT APPLICATION NUMBER: US/10/261,164
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-164-1

Query Match      99.9%; Score 6098; DB 15; Length 1170;
Best Local Similarity 99.9%; Pred. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      121 ONTYLSGICVLFROMLOQPMLOGRPGFOEICKGNVDLVFLPDGSMILOPDEFOKILDPMK 180
Db      121 ONTYLSGICVLFROMLOQPMLOGRPGFOEICKGNVDLVFLPDGSMILOPDEFOKILDPMK 180
Qy      181 DVMKGLSNTSYQFAAVOFSSTYKTEPDFSDVKKKDDPDLAKHYKMLLNTNGAINVY 240
Db      181 DVMKGLSNTSYQFAAVOFSSTYKTEPDFSDVKKKDDPDLAKHYKMLLNTNGAINVY 240
Qy      241 ATEVFRBELGARPDATKVLIIITDGEATDGSNIDAANDIIRYIIIGIKHFQTKESQETLH 300
Db      241 ATEVFRBELGARPDATKVLIIITDGEATDGSNIDAANDIIRYIIIGIKHFQTKESQETLH 300
Qy      301 KPAKSPASEFYKIIDTEBKLDLFELOKTIYVEGTSKODLTSPNNELSSGSIADLSR 360
Db      301 KPAKSPASEFYKIIDTEBKLDLFELOKTIYVEGTSKODLTSPNNELSSGSIADLSR 360
Qy      361 GHAVVAVGAKOMWAGGFLDLKADLQDDPTFIGNELTPEVRAGYLYGYTWTMLPSROKTSIL 420
Db      361 GHAVVAVGAKOMWAGGFLDLKADLQDDPTFIGNELTPEVRAGYLYGYTWTMLPSROKTSIL 420
Qy      421 ASGARVYOHMGRVLLFQEPQGGHMSQVOTIHGTQISYFGBELCGVDVDDGETELLLI 480
Db      421 ASGARVYOHMGRVLLFQEPQGGHMSQVOTIHGTQISYFGBELCGVDVDDGETELLLI 480
Qy      481 GAPLFYGBORGRVFIYQRRQLGFEVSELOQDPGYLGRFGELITALTDINGGLYDVA 540
Db      481 GAPLFYGBORGRVFIYQRRQLGFEVSELOQDPGYLGRFGELITALTDINGGLYDVA 540
Qy      541 VGAPLEBQAGAYIFNGRHGGLSPQPSQRILEGTVLSGIQMFGRSIHGVLKDEGDLADVA 600
Db      541 VGAPLEBQAGAYIFNGRHGGLSPQPSQRILEGTVLSGIQMFGRSIHGVLKDEGDLADVA 600
Qy      601 VGASEQMTVLSRRPVVDWMTLMSSEPAIIPVHEVCSTSTSNKMEGVNITICFOIKSLY 660
Db      601 VGASEQMTVLSRRPVVDWMTLMSSEPAIIPVHEVCSTSTSNKMEGVNITICFOIKSLY 660
Qy      661 POFQGRIVANITVTLQLDGHRTRRGLPPGGHRLRNIAVTTSMSCDTFSFHPVCQD 720
Db      661 POFQGRIVANITVTLQLDGHRTRRGLPPGGHRLRNIAVTTSMSCDTFSFHPVCQD 720
Qy      721 LISPIVSLNFSLMBEETPRDQAOQKDIPIILPRLSHSTWEIIPFEKNGCEDKCCAN 780
Db      721 LISPIVSLNFSLMBEETPRDQAOQKDIPIILPRLSHSTWEIIPFEKNGCEDKCCAN 780
Qy      781 LRVSPSPARSRLRLTAFASLSVELSLNLEEDAVWQDLHPFGLSFRKYEMLKPHSQ 840
Db      781 LRVSPSPARSRLRLTAFASLSVELSLNLEEDAVWQDLHPFGLSFRKYEMLKPHSQ 840
Qy      841 IPVSCBELPEBSRLSLRSLSCNVSSPIFKAGSHVALQMMFNTLVNNSWGSDELHANTC 900
Db      841 IPVSCBELPEBSRLSLRSLSCNVSSPIFKAGSHVALQMMFNTLVNNSWGSDELHANTC 900
Qy      901 NNEDSDLEEDNSATITIPILYPINILIQOEDSTLYVSTFKPKGIHQVKMYQVRIOPS 960
Db      901 NNEDSDLEEDNSATITIPILYPINILIQOEDSTLYVSTFKPKGIHQVKMYQVRIOPS 960
Qy      961 IHDNIPITLBAVVGVPQPSSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGALFR 1020
Db      961 IHDNIPITLBAVVGVPQPSSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGALFR 1020
Qy      1021 CPVVRQELIVQVITGLTLEVGELIEMSMFSLCSSLSTISFNSSKHHLVGSNASLAQVVMK 1080
Db      1021 CPVVRQELIVQVITGLTLEVGELIEMSMFSLCSSLSTISFNSSKHHLVGSNASLAQVVMK 1080
Qy      1081 VDVIYKEMQMLYLYVLSIGILLLLIFIVLYKVGFFRKNLKEKMEAGRGVNGI PAEDS 1140
Db      1081 VDVIYKEMQMLYLYVLSIGILLLLIFIVLYKVGFFRKNLKEKMEAGRGVNGI PAEDS 1140
Qy      1141 EQLASGEADGPGCLKPLHEKDSSEGGKD 1170
Db      1141 EQLASGEADGPGCLKPLHEKDSSEGGKD 1170

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RESULT 4  
US-10-473-127-1737  
; Sequence 1737, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1737  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1737

Query Match 99.9%; Score 6098; DB 16; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MKDSCITYAMALLSGFFFAFPASSYNDVGRARSFSPRAGRHRFGYVLOVGVNGVIYGA 60
DB      1 MKDSCITYAMALLSGFFFAFPASSYNDVGRARSFSPRAGRHRFGYVLOVGVNGVIYGA 60
QY      61 PGEKNGSTSLYQCCSGTGHCLPYTLRGSNYTSKYLGMTLADPTDGSILACDPGLSRCD 120
DB      61 PGEKNGSTSLYQCCSGTGHCLPYTLRGSNYTSKYLGMTLADPTDGSILACDPGLSRCD 120
QY      121 QNTYLSGLCYLFRONLQGPMLQGRPGFQCKIGANDVLELFDGSMSLQPDFQKILDFMK 180
DB      121 QNTYLSGLCYLFRONLQGPMLQGRPGFQCKIGANDVLELFDGSMSLQPDFQKILDFMK 180
QY      181 DVMKLSNTSYQFAAVQFSTSYKTEPFDSDYKRDPPALLKRVKMLLNTFGAINVY 240
DB      181 DVMKLSNTSYQFAAVQFSTSYKTEPFDSDYKRDPPALLKRVKMLLNTFGAINVY 240
QY      241 ATEVREBELGARPDATKYLIIITTOEANDSGNIDAKOIIIRIIGIGHFQTKESQETLH 300
DB      241 ATEVREBELGARPDATKYLIIITTOEANDSGNIDAKOIIIRIIGIGHFQTKESQETLH 300
QY      301 KFAKSPASEFYKIDTFEKLKDLFTLQKTIYVIGTSKODLTSFNMELSSGSIADLSR 360
DB      301 KFAKSPASEFYKIDTFEKLKDLFTLQKTIYVIGTSKODLTSFNMELSSGSIADLSR 360
QY      361 GHAAVAVGAGDWMAGFLDLKADLDDTFIIGNEPLTFPEVRAGYLGITYTWMLEPSRKTSLL 420
DB      361 GHAAVAVGAGDWMAGFLDLKADLDDTFIIGNEPLTFPEVRAGYLGITYTWMLEPSRKTSLL 420
QY      421 ASGARVYQHMGRVILLFOEPQGGHMSOVQTHGTOIGSYFGSELGQUNVDDQETELLII 480
DB      421 ASGARVYQHMGRVILLFOEPQGGHMSOVQTHGTOIGSYFGSELGQUNVDDQETELLII 480
QY      481 GAPLFYGEORGGRVFIYORROLGFEEVESELQDPGYPLGRFGEATLTALTDINGDLVYA 540
DB      481 GAPLFYGEORGGRVFIYORROLGFEEVESELQDPGYPLGRFGEATLTALTDINGDLVYA 540
QY      541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDGLADVA 600
DB      541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDGLADVA 600
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DB      541 VGAPLEEGGAVYIFNGRHGGLSPQPSQRIEGTVLSGIQWFGRSIHGVKDLBGDGLADVA 600
QY      601 VGAESOMITVLSRPVVMYTLMSGSPAEIPVHEKCSYTSNMKEGVNTTICFOIKSLY 660
DB      601 VGAESOMITVLSRPVVMYTLMSGSPAEIPVHEKCSYTSNMKEGVNTTICFOIKSLY 660
QY      661 PQFQGRIVANLTYTLQDGHRTTRRGFLPGGRHRLRNIAVTTSMSCTDPSFHFVPCVD 720
DB      661 PQFQGRIVANLTYTLQDGHRTTRRGFLPGGRHRLRNIAVTTSMSCTDPSFHFVPCVD 720
QY      721 LISPINVSLNPSLMEEGTPTDQAGKDIPIILRPSLSEETWBIPEPKNGEDKCEAN 780
DB      721 LISPINVSLNPSLMEEGTPTDQAGKDIPIILRPSLSEETWBIPEPKNGEDKCEAN 780
QY      781 LRVSFSPARARALRTAFASLVELSLSNLEBDAVWQLDHPPGISFPRKVMLEKPHSQ 840
DB      781 LRVSFSPARARALRTAFASLVELSLSNLEBDAVWQLDHPPGISFPRKVMLEKPHSQ 840
QY      841 IPVSCEBLPEBSRLSLRSLSCNVSSPIFKAGHSVALQMFNTLVNSSWGDSEIHAHVTC 900
DB      841 IPVSCEBLPEBSRLSLRSLSCNVSSPIFKAGHSVALQMFNTLVNSSWGDSEIHAHVTC 900
QY      901 NNEDSDLEEDNSATTTIPIIYPINILIQDQDSTLYVSFTPKGPKIHQVGMTQVRIQPS 960
DB      901 NNEDSDLEEDNSATTTIPIIYPINILIQDQDSTLYVSFTPKGPKIHQVGMTQVRIQPS 960
QY      961 IHDNITPLEAVYGVPOPSPSGPITTHOWSVQMPVPCHEDELRDLPAEPCLPGALFR 1020
DB      961 IHDNITPLEAVYGVPOPSPSGPITTHOWSVQMPVPCHEDELRDLPAEPCLPGALFR 1020
QY      1021 CPVFEROELLIVQVIGTLELVGEIEASSMFSLSISLISFNSSKHFLYGSNASLAQVVMK 1080
DB      1021 CPVFEROELLIVQVIGTLELVGEIEASSMFSLSISLISFNSSKHFLYGSNASLAQVVMK 1080
QY      1081 VDVYTERQMTLYLTLGIGLLLLLFYLYKYVFFKRNULKEXMEAGRGVPGNIPAEBS 1140
DB      1081 VDVYTERQMTLYLTLGIGLLLLLFYLYKYVFFKRNULKEXMEAGRGVPGNIPAEBS 1140
QY      1141 EQLASGQEGADPGCLKPLHKDSBSGGKD 1170
DB      1141 EQLASGQEGADPGCLKPLHKDSBSGGKD 1170
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RESULT 5  
US-10-473-127-1739  
; Sequence 1739, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1739  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1739

Query Match 99.9%; Score 6098; DB 16; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITWAMALLSGFFFPASSYNLDVGRASFSPPRAGRHFGRVLDVGVGVYGA 60  
 DB 1 MKDSCITWAMALLSGFFFPASSYNLDVGRASFSPPRAGRHFGRVLDVGVGVYGA 60  
 QY 61 PEGNGSTSLVYOCOSGTGCHLPVTLRGSNTSKYLGMTLATDPTDGSILACDPSRTCD 120  
 DB 61 PEGNGSTSLVYOCOSGTGCHLPVTLRGSNTSKYLGMTLATDPTDGSILACDPSRTCD 120  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQPDFOKILDPMK 180  
 DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQPDFOKILDPMK 180  
 QY 181 DVMKLSTNTSYQFAAVOSTSYKTEFSDVYKRDPAALKHVGHMLLTNTFGAINVY 240  
 DB 181 DVMKLSTNTSYQFAAVOSTSYKTEFSDVYKRDPAALKHVGHMLLTNTFGAINVY 240  
 QY 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAAKOIIRYIIGIGHFQTKESQETLH 300  
 DB 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAAKOIIRYIIGIGHFQTKESQETLH 300  
 QY 301 KPASKPASEFVKILDTPEKLDLFTLEOKIYVIEGTSKODLTSFMNELSSGISADLSR 360  
 DB 301 KPASKPASEFVKILDTPEKLDLFTLEOKIYVIEGTSKODLTSFMNELSSGISADLSR 360  
 QY 361 GHAVAVGAKDMAGFLDLKADLDDPTFIGNEPLEPRAGYLGVTWMLPSRQKSTLL 420  
 DB 361 GHAVAVGAKDMAGFLDLKADLDDPTFIGNEPLEPRAGYLGVTWMLPSRQKSTLL 420  
 QY 421 ASGADRYOHMGVILLFOEPQGGGSHSVQVTHGTQIGSYFGGELCGVDVDDGKTELLLI 480  
 DB 421 ASGADRYOHMGVILLFOEPQGGGSHSVQVTHGTQIGSYFGGELCGVDVDDGKTELLLI 480  
 QY 481 GAPIFYGROGRGRVITYORROIGFEFVESELODPEYPLGRFEBATLTALTDINGDLVYVA 540  
 DB 481 GAPIFYGROGRGRVITYORROIGFEFVESELODPEYPLGRFEBATLTALTDINGDLVYVA 540  
 QY 541 VGAPLEBOGAVYIFNGRHGSLSPQSORLEGTOVLSGIOMFGRSHGVYLEDGDLAVYA 600  
 DB 541 VGAPLEBOGAVYIFNGRHGSLSPQSORLEGTOVLSGIOMFGRSHGVYLEDGDLAVYA 600  
 QY 601 VGASQOMTVLSSRPVVDWVTLMSFSPAIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
 DB 601 VGASQOMTVLSSRPVVDWVTLMSFSPAIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
 QY 661 POFQORLVANLTYTQLODGHRTTRRGGLPFGGRHBLRRNIAVTTSMSCCTDFSFHPVCVOD 720  
 DB 661 POFQORLVANLTYTQLODGHRTTRRGGLPFGGRHBLRRNIAVTTSMSCCTDFSFHPVCVOD 720  
 QY 721 LIISPINVSINFSLMBEEGTPRDORAQKODIPILRPSLSHSETWEIPEFKNCEDEKCCAN 780  
 DB 721 LIISPINVSINFSLMBEEGTPRDORAQKODIPILRPSLSHSETWEIPEFKNCEDEKCCAN 780  
 QY 781 LRVSPSPARSRLRLTAFASSLVELSLNLEBEDAYVOLDLHFPGLSFRKYEMLKPHSQ 840  
 DB 781 LRVSPSPARSRLRLTAFASSLVELSLNLEBEDAYVOLDLHFPGLSFRKYEMLKPHSQ 840  
 QY 841 IPVSEEBELPESRRLSLRALSQVSSPIFKAQSHVALQMMFNTLVNNSGDSVELHANTYC 900  
 DB 841 IPVSEEBELPESRRLSLRALSQVSSPIFKAQSHVALQMMFNTLVNNSGDSVELHANTYC 900  
 QY 901 NNHBDLLEDNSATTIIPILYPINILIDQOEDSTLYVSPTPKGPRIHOKHMYOYRIOPS 960  
 DB 901 NNHBDLLEDNSATTIIPILYPINILIDQOEDSTLYVSPTPKGPRIHOKHMYOYRIOPS 960  
 QY 961 IHDHNIPTLEAVVGVQPPSEGPITHQSVQMBPVPCYHEDLERLPDAAECLPGLALFR 1020  
 DB 961 IHDHNIPTLEAVVGVQPPSEGPITHQSVQMBPVPCYHEDLERLPDAAECLPGLALFR 1020  
 QY 1021 CPVVRQELIVQVIGTLELVEIEASMSFSLCSSISIFNSKHFHLYGSNASTLAQVYMK 1080

DB 1021 CPVVRQELIVQVIGTLELVEIEASMSFSLCSSISIFNSKHFHLYGSNASTLAQVYMK 1080  
 QY 1081 VDVIYERKOMLYLYLSGIGLILLLLIFVLVYKVGFFGRNLIKERMEAGRGVPGNIPADS 1140  
 DB 1081 VDVIYERKOMLYLYLSGIGLILLLLIFVLVYKVGFFGRNLIKERMEAGRGVPGNIPADS 1140  
 QY 1141 EQLASGQAGDPGCLKPLHEKDSSEGGKD 1170  
 DB 1141 EQLASGQAGDPGCLKPLHEKDSSEGGKD 1170

RESULT 6  
 US-10-473-127-1742  
 ; Sequence 1742, Application US/10473127  
 ; Publication No. US20040236091A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zycoo Inc.  
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
 ; FILE REFERENCE: 08191-026W01  
 ; CURRENT APPLICATION NUMBER: US/10/473,127  
 ; CURRENT FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: 60/279,495  
 ; PRIOR FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: 60/292,544  
 ; PRIOR FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: 60/310,801  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: 60/326,370  
 ; PRIOR FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: 60/336,780  
 ; PRIOR FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: 60/358,985  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 2041  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO: 1742  
 ; LENGTH: 1170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-473-127-1742

Query Match 99.9%; Score 6098; DB 16; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITWAMALLSGFFFPASSYNLDVGRASFSPPRAGRHFGRVLDVGVGVYGA 60  
 DB 1 MKDSCITWAMALLSGFFFPASSYNLDVGRASFSPPRAGRHFGRVLDVGVGVYGA 60  
 QY 61 PEGNGSTSLVYOCOSGTGCHLPVTLRGSNTSKYLGMTLATDPTDGSILACDPSRTCD 120  
 DB 61 PEGNGSTSLVYOCOSGTGCHLPVTLRGSNTSKYLGMTLATDPTDGSILACDPSRTCD 120  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQPDFOKILDPMK 180  
 DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQPDFOKILDPMK 180  
 QY 181 DVMKLSTNTSYQFAAVOSTSYKTEFSDVYKRDPAALKHVGHMLLTNTFGAINVY 240  
 DB 181 DVMKLSTNTSYQFAAVOSTSYKTEFSDVYKRDPAALKHVGHMLLTNTFGAINVY 240  
 QY 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAAKOIIRYIIGIGHFQTKESQETLH 300  
 DB 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAAKOIIRYIIGIGHFQTKESQETLH 300  
 QY 301 KPASKPASEFVKILDTPEKLDLFTLEOKIYVIEGTSKODLTSFMNELSSGISADLSR 360  
 DB 301 KPASKPASEFVKILDTPEKLDLFTLEOKIYVIEGTSKODLTSFMNELSSGISADLSR 360  
 QY 361 GHAVAVGAKDMAGFLDLKADLDDPTFIGNEPLEPRAGYLGVTWMLPSRQKSTLL 420  
 DB 361 GHAVAVGAKDMAGFLDLKADLDDPTFIGNEPLEPRAGYLGVTWMLPSRQKSTLL 420

QY 421 ASGARPYOHMGRVLLFOEPQGGHMSQVQTHGTQISYFGGELCGVVDODGETELLII 480  
DB 421 ASGARPYOHMGRVLLFOEPQGGHMSQVQTHGTQISYFGGELCGVVDODGETELLII 480  
QY 481 GAPLFYGOGRGRVFIYORRQLGFEVESELQDPCGYGRGFEATLTDINGDLVVA 540  
DB 481 GAPLFYGOGRGRVFIYORRQLGFEVESELQDPCGYGRGFEATLTDINGDLVVA 540  
QY 541 VGAPLEBOGAVYIFNGRHGSLSPQSORIEGTQVLSGIOMFGRSIHGVKDEGDLAVA 600  
DB 541 VGAPLEBOGAVYIFNGRHGSLSPQSORIEGTQVLSGIOMFGRSIHGVKDEGDLAVA 600  
QY 601 VGASQMTVLSSRPVDMVTLLMSFSPAEIPVHEVCSTYSNKKMEGVNITICQIKSLY 660  
DB 601 VGASQMTVLSSRPVDMVTLLMSFSPAEIPVHEVCSTYSNKKMEGVNITICQIKSLY 660  
QY 661 POFQGRIVANLTYTLQDGHRTTRRGLFPGGRHRLRNIAVTTSMSCDPSFHPVCVD 720  
DB 661 POFQGRIVANLTYTLQDGHRTTRRGLFPGGRHRLRNIAVTTSMSCDPSFHPVCVD 720  
QY 721 LISPINVSLNFSLMBEETPRDQAGKDIPIILRPSLHSETWEIIPREKNGCEDKKEAN 780  
DB 721 LISPINVSLNFSLMBEETPRDQAGKDIPIILRPSLHSETWEIIPREKNGCEDKKEAN 780  
QY 781 LRVSPSPARSRLRLTAFASLSVELSLSNLEBDAYWQDLHFPGLSFRKVEMLKPHSQ 840  
DB 781 LRVSPSPARSRLRLTAFASLSVELSLSNLEBDAYWQDLHFPGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCEBEPBESRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSMGDSVELHANVC 900  
DB 841 IPVSCEBEPBESRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSMGDSVELHANVC 900  
QY 901 NNEBSDLIEDNSATTIIPILYPINLIDQEDSTLYSFTPKGPIHVKMYOVRIOPS 960  
DB 901 NNEBSDLIEDNSATTIIPILYPINLIDQEDSTLYSFTPKGPIHVKMYOVRIOPS 960  
QY 961 IHDNIPITLEAVGVQPPSEGPITTHQMSVOMEPPVPCHEDELERLDAAPCPLGALFR 1020  
DB 961 IHDNIPITLEAVGVQPPSEGPITTHQMSVOMEPPVPCHEDELERLDAAPCPLGALFR 1020  
QY 1021 CPVVFROBILVQVIGTLELVEIEASSMFSLCSISIFNSSKHFHLVGSNASLAQVVMK 1080  
DB 1021 CPVVFROBILVQVIGTLELVEIEASSMFSLCSISIFNSSKHFHLVGSNASLAQVVMK 1080  
QY 1081 DVVVEKQMLTYLVSIGLGLLLLLIFLYLYKVGFPFRNLKEKMEAGRGVNGIPEADS 1140  
DB 1081 DVVVEKQMLTYLVSIGLGLLLLLIFLYLYKVGFPFRNLKEKMEAGRGVNGIPEADS 1140  
QY 1141 EQLASGOEAGDPCGLKPLHEKXDSGSGKD 1170  
DB 1141 EQLASGOEAGDPCGLKPLHEKXDSGSGKD 1170  
RESULT 7  
US-10-741-600-1088  
; Sequence 1088, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1088  
; LENGTH: 1170  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-741-600-1088

Query Match 99.9%; Score 6098; DB 17; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKDSCITVMAALLSGFFPFPAPASSTYLDVGRARSFSPAPAGRRVTVQVNGVTVGA 60  
DB 1 MKDSCITVMAALLSGFFPFPAPASSTYLDVGRARSFSPAPAGRRVTVQVNGVTVGA 60  
QY 61 PGEAGNSTGSLYQCCSGTGCLPVTLRGSNTYSKILGNTLTATPDGSIILACDPGLSRCTD 120  
DB 61 PGEAGNSTGSLYQCCSGTGCLPVTLRGSNTYSKILGNTLTATPDGSIILACDPGLSRCTD 120  
QY 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFOECIKGNVDLVFLPDGSMILOPDEFQKILDFMK 180  
DB 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFOECIKGNVDLVFLPDGSMILOPDEFQKILDFMK 180  
QY 181 DVMKCLSNSTSYQFAAVOPSTSYKTEFPSPDYVRKDPDALLKRYKMLLTNTFGALNV 240  
DB 181 DVMKCLSNSTSYQFAAVOPSTSYKTEFPSPDYVRKDPDALLKRYKMLLTNTFGALNV 240  
QY 241 ATEVFREELGARPPATKYLIIITDGEATDGNIDAAKOIRYIIGIKHPQTKESQETLH 300  
DB 241 ATEVFREELGARPPATKYLIIITDGEATDGNIDAAKOIRYIIGIKHPQTKESQETLH 300  
QY 301 KFASKPASEFYKIIDTEBKLDFTELQKKIYVIEGTSKODLISFNNELSSSGISADLSR 360  
DB 301 KFASKPASEFYKIIDTEBKLDFTELQKKIYVIEGTSKODLISFNNELSSSGISADLSR 360  
QY 361 GHAVVAVGAKDWAAGSLDLKADLQDDPTFGNEBLTEBVAAGTYGVVWMLPSQKXSL 420  
DB 361 GHAVVAVGAKDWAAGSLDLKADLQDDPTFGNEBLTEBVAAGTYGVVWMLPSQKXSL 420  
QY 421 ASGARPYOHMGRVLLFOEPQGGHMSQVQTHGTQISYFGGELCGVVDODGETELLII 480  
DB 421 ASGARPYOHMGRVLLFOEPQGGHMSQVQTHGTQISYFGGELCGVVDODGETELLII 480  
QY 481 GAPLFYGOGRGRVFIYORRQLGFEVESELQDPCGYGRGFEATLTDINGDLVVA 540  
DB 481 GAPLFYGOGRGRVFIYORRQLGFEVESELQDPCGYGRGFEATLTDINGDLVVA 540  
QY 541 VGAPLEBOGAVYIFNGRHGSLSPQSORIEGTQVLSGIOMFGRSIHGVKDEGDLAVA 600  
DB 541 VGAPLEBOGAVYIFNGRHGSLSPQSORIEGTQVLSGIOMFGRSIHGVKDEGDLAVA 600  
QY 601 VGASQMTVLSSRPVDMVTLLMSFSPAEIPVHEVCSTYSNKKMEGVNITICQIKSLY 660  
DB 601 VGASQMTVLSSRPVDMVTLLMSFSPAEIPVHEVCSTYSNKKMEGVNITICQIKSLY 660  
QY 661 POFQGRIVANLTYTLQDGHRTTRRGLFPGGRHRLRNIAVTTSMSCDPSFHPVCVD 720  
DB 661 POFQGRIVANLTYTLQDGHRTTRRGLFPGGRHRLRNIAVTTSMSCDPSFHPVCVD 720  
QY 721 LISPINVSLNFSLMBEETPRDQAGKDIPIILRPSLHSETWEIIPREKNGCEDKKEAN 780  
DB 721 LISPINVSLNFSLMBEETPRDQAGKDIPIILRPSLHSETWEIIPREKNGCEDKKEAN 780  
QY 781 LRVSPSPARSRLRLTAFASLSVELSLSNLEBDAYWQDLHFPGLSFRKVEMLKPHSQ 840  
DB 781 LRVSPSPARSRLRLTAFASLSVELSLSNLEBDAYWQDLHFPGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCEBEPBESRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSMGDSVELHANVC 900  
DB 841 IPVSCEBEPBESRLLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSMGDSVELHANVC 900  
QY 901 NNEBSDLIEDNSATTIIPILYPINLIDQEDSTLYSFTPKGPIHVKMYOVRIOPS 960  
DB 901 NNEBSDLIEDNSATTIIPILYPINLIDQEDSTLYSFTPKGPIHVKMYOVRIOPS 960  
QY 961 IHDNIPITLEAVGVQPPSEGPITTHQMSVOMEPPVPCHEDELERLDAAPCPLGALFR 1020  
DB 961 IHDNIPITLEAVGVQPPSEGPITTHQMSVOMEPPVPCHEDELERLDAAPCPLGALFR 1020  
QY 1021 CPVVFROBILVQVIGTLELVEIEASSMFSLCSISIFNSSKHFHLVGSNASLAQVVMK 1080

```

Db      1021 CQVVERQELIVQVIGTLELVGEIEASMSWLSLSSISISKHHLYSNA5LAQVYMK 1080
Qy      1081 VDVYTERKOMLYLYLSGIGGLLLLIIFLYLYKVGFFKRNLEKKEAGRGVNGI PAEDS 1140
Db      1081 VDVYTERKOMLYLYLSGIGGLLLLIIFLYLYKVGFFKRNLEKKEAGRGVNGI PAEDS 1140
Qy      1141 EQLASGQEGADPGCLKPLHEKDESGGKD 1170
Db      1141 EQLASGQEGADPGCLKPLHEKDESGGKD 1170

```

## RESULT 8

```

US-11-062-290-1
; Sequence 1, Application US/11062290
; Publication No. US20050142134A1
; GENERAL INFORMATION:
; APPLICANT: KAPUSTAY, PAMELA M.
; APPLICANT: LEWIS, REX H.
; TITLE OF INVENTION: LFA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: 046007/0272304
; CURRENT APPLICATION NUMBER: US/11/062,290
; PRIOR FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/10/261,164
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-062-290-1

```

```

Query Match      99.9%; Score 6098; DB 20; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MKDSCITVAMALLSGFFFPASSYNLDVGRASFSPPRAGRHFGRVLYQVNGVIVGA 60
Db      1 MKDSCITVAMALLSGFFFPASSYNLDVGRASFSPPRAGRHFGRVLYQVNGVIVGA 60
Qy      61 PEGNSSTSLVQCOSGTGHCPLVTLRGSNVTSKYLGMTLATDPTDGSILACPGISRTCD 120
Db      61 PEGNSSTSLVQCOSGTGHCPLVTLRGSNVTSKYLGMTLATDPTDGSILACPGISRTCD 120
Qy      121 QNTVLSGLCYLFRQLQCPMLQGRPGFOECIKGNVLYLFPDGSMSLOPDEFQKILDFMK 180
Db      121 QNTVLSGLCYLFRQLQCPMLQGRPGFOECIKGNVLYLFPDGSMSLOPDEFQKILDFMK 180
Qy      181 DVNKKLSNTSYQFAAVQFSTSYKTEFSDYVYKRDPAALLKRVKRMLLTNTFGAINVY 240
Db      181 DVNKKLSNTSYQFAAVQFSTSYKTEFSDYVYKRDPAALLKRVKRMLLTNTFGAINVY 240
Qy      241 ATTVREBELGARPDATKYLIIITDDEATDSGNIDAAKDIIRITIGIGKHFQKESQETLH 300
Db      241 ATTVREBELGARPDATKYLIIITDDEATDSGNIDAAKDIIRITIGIGKHFQKESQETLH 300
Qy      301 KFAKSPASEFVYLITFEKLKDLFTELQKIYVIGTSGKODLTSFMELSSSGISADLSR 360
Db      301 KFAKSPASEFVYLITFEKLKDLFTELQKIYVIGTSGKODLTSFMELSSSGISADLSR 360
Qy      361 GHAVVGAAGAKMAGGFLDLKADLDDFTIGNEPLTPREVAGYLYGVYTWLPSRQKTSLL 420
Db      361 GHAVVGAAGAKMAGGFLDLKADLDDFTIGNEPLTPREVAGYLYGVYTWLPSRQKTSLL 420
Qy      421 ASGARRYQMGHGVLLFQEPQGGGHSQVOTIHGTQISYFGEELGCVNDVDDGRTLELLI 480
Db      421 ASGARRYQMGHGVLLFQEPQGGGHSQVOTIHGTQISYFGEELGCVNDVDDGRTLELLI 480
Qy      481 GAPLFYGEORGRGVLYQRRQLGFEEVSELODPCGYLGRFGEAITALTIDINGDGLVYA 540
Db      481 GAPLFYGEORGRGVLYQRRQLGFEEVSELODPCGYLGRFGEAITALTIDINGDGLVYA 540

```

```

Qy      541 VGAPLEBQAGYVIFNGRHGSLSPQSORIEGNOVLSGIQWFGRSIHGYKDLBGDLADVA 600
Db      541 VGAPLEBQAGYVIFNGRHGSLSPQSORIEGNOVLSGIQWFGRSIHGYKDLBGDLADVA 600
Qy      601 VGASOMIVLSRPVMDVMTLMSFSPAEI PVHEVECSYSTSNKKEGVNITICFOIKSLY 660
Db      601 VGASOMIVLSRPVMDVMTLMSFSPAEI PVHEVECSYSTSNKKEGVNITICFOIKSLY 660
Qy      661 POFQGRVLANITTYLQLDGHRTRRGGLFPGGRHLEKRNIAVTTSMCTDSFHHFVYQD 720
Db      661 POFQGRVLANITTYLQLDGHRTRRGGLFPGGRHLEKRNIAVTTSMCTDSFHHFVYQD 720
Qy      721 LISPIVNSLWSEBEGTPRDQAGKDIPILLRPSLHSTWELPEKNGGEQDKCAN 780
Db      721 LISPIVNSLWSEBEGTPRDQAGKDIPILLRPSLHSTWELPEKNGGEQDKCAN 780
Qy      781 LRVSPARSRLRLTAPASLSVELSLNLEDAVWQDLHFPGLSFRKVMKLPKPSQ 840
Db      781 LRVSPARSRLRLTAPASLSVELSLNLEDAVWQDLHFPGLSFRKVMKLPKPSQ 840
Qy      841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAGHVALQMMFNTLVNSMGDSVELHANVTC 900
Db      841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAGHVALQMMFNTLVNSMGDSVELHANVTC 900
Qy      901 NNEBSDLIEDNSATTIIPILYPINILIODQEDSTLYSFTKGPRIHOVKMYOVRIOPS 960
Db      901 NNEBSDLIEDNSATTIIPILYPINILIODQEDSTLYSFTKGPRIHOVKMYOVRIOPS 960
Qy      961 IHDNIPTLEAVGVQPPSEGPITTHQMSVQMEPPVPCHEYEDLERLPAAEPCLPALFR 1020
Db      961 IHDNIPTLEAVGVQPPSEGPITTHQMSVQMEPPVPCHEYEDLERLPAAEPCLPALFR 1020
Qy      1021 CPVVERQELIVQVIGTLELVGEIEASMSWLSLSSISISKHHLYSNA5LAQVYMK 1080
Db      1021 CPVVERQELIVQVIGTLELVGEIEASMSWLSLSSISISKHHLYSNA5LAQVYMK 1080
Qy      1081 VDVYTERKOMLYLYLSGIGGLLLLIIFLYLYKVGFFKRNLEKKEAGRGVNGI PAEDS 1140
Db      1081 VDVYTERKOMLYLYLSGIGGLLLLIIFLYLYKVGFFKRNLEKKEAGRGVNGI PAEDS 1140
Qy      1141 EQLASGQEGADPGCLKPLHEKDESGGKD 1170
Db      1141 EQLASGQEGADPGCLKPLHEKDESGGKD 1170

```

## RESULT 9

```

US-10-741-600-1086
; Sequence 1086, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1086
; LENGTH: 1223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1086

```

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Query Match      99.3%; Score 6061.5; DB 17; Length 1223;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 53; Gaps 1;

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```

Qy      1 MKDSCITVAMALLSGFFFPASSYNLDVGRASFSPPRAGRHFGRVLYQVNGVIVGA 60
Db      1 MKDSCITVAMALLSGFFFPASSYNLDVGRASFSPPRAGRHFGRVLYQVNGVIVGA 60
Qy      61 PEGNSSTSLVQCOSGTGHCPLVTLRGSNVTSKYLGMTLATDPTDGSILACPGISRTCD 120

```



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Db      61  PGEKNSGSLYOCOSGTHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Qy      121  QNTYLSGICYLFRONLQGRPGROECIKGNVDLVFLPDGSMLOPDEFQKILDFMK 180
Db      121  QNTYLSGICYLFRONLQGRPGROECIKGNVDLVFLPDGSMLOPDEFQKILDFMK 180
Qy      181  DVMKLSNTSYQFAAVQSTSYKTEFPDSYVKRDPALLKHYKHMILLNTFGAINVY 240
Db      181  DVMKLSNTSYQFAAVQSTSYKTEFPDSYVKRDPALLKHYKHMILLNTFGAINVY 240
Qy      241  ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIKHFQTKESQETLH 300
Db      241  ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIKHFQTKESQETLH 300
Qy      301  KPASKPASEPVKIIDTEBEKLDLFTLEOKKIYVIEGTSKODLTSNNMELSSSGISADLSR 360
Db      301  KPASKPASEPVKIIDTEBEKLDLFTLEOKKIYVIEGTSKODLTSNNMELSSSGISADLSR 360
Qy      361  GHAVVAVGAKDMAGGFLDKADLQDDTFIGNEBLTPBEVAGYLGIVTWMPSROKTSIL 420
Db      361  GHAVVAVGAKDMAGGFLDKADLQDDTFIGNEBLTPBEVAGYLGIVTWMPSROKTSIL 420
Qy      421  ASGAPRYOHMGRVILLFQEPQGGHWSQVQTHGTQISYFGGELCGVDVDDGETELLII 480
Db      421  ASGAPRYOHMGRVILLFQEPQGGHWSQVQTHGTQISYFGGELCGVDVDDGETELLII 480
Qy      481  GAPLFYGBORGGRVFIYORROLGFEVESELODPPYLGIRGEGALTALTDINGGLVDA 540
Db      481  GAPLFYGBORGGRVFIYORROLGFEVESELODPPYLGIRGEGALTALTDINGGLVDA 540
Qy      541  VGAPLEBOGAVYIFNGRHGGLSPQSPQRIEQTQVLSGIQWFGRSIHGVKLEGDGLADVA 600
Db      541  VGAPLEBOGAVYIFNGRHGGLSPQSPQRIEQTQVLSGIQWFGRSIHGVKLEGDGLADVA 600
Qy      601  VGASQMTVLSSRPVDMWTLMSPSPAI PVHEVCSYSTSNKMEGVNITTCFOIKSLY 660
Db      601  VGASQMTVLSSRPVDMWTLMSPSPAI PVHEVCSYSTSNKMEGVNITTCFOIKSLY 660
Qy      661  POFQRLVANIYTLTQLDGHRTRRGLFPGRHELRNIAVTSMSCDPSFHPVVCOD 720
Db      661  POFQRLVANIYTLTQLDGHRTRRGLFPGRHELRNIAVTSMSCDPSFHPVVCOD 720
Qy      721  LISPIVNSLNSLWEEBGTPRDQRAQKDIPIILRPSLHSETWLPPEKNCGEKKCBAN 780
Db      721  LISPIVNSLNSLWEEBGTPRDQRAQKDIPIILRPSLHSETWLPPEKNCGEKKCBAN 780
Qy      781  LRVFSPPARSRLRTAFASLSVELSLNLEEDAYVQDLHFPFGLSFRKVEMLKPSHQ 840
Db      781  LRVFSPPARSRLRTAFASLSVELSLNLEEDAYVQDLHFPFGLSFRKVEMLKPSHQ 840
Qy      841  IPVGEELPESSRLSLALSCVSPPIKAGHSVALQWMTVLNNSMGDSVELHANTYC 900
Db      841  IPVGEELPESSRLSLALSCVSPPIKAGHSVALQWMTVLNNSMGDSVELHANTYC 900
Qy      901  NNEBSDLLEDSATTIIPILVPINLLIDQDSESTLYSFTPGKPIHGVKNHYO----- 954
Db      901  NNEBSDLLEDSATTIIPILVPINLLIDQDSESTLYSFTPGKPIHGVKNHYO----- 954
Qy      955  -----VRIQPSIHNDNI 967
Db      955  -----VRIQPSIHNDNI 967
Qy      961  EMQTSKQILCRPADAEHTVGAQEBELPCPMGVSEAFRDNIRAGPCRVRIQPSIHNDNI 1020
Db      961  EMQTSKQILCRPADAEHTVGAQEBELPCPMGVSEAFRDNIRAGPCRVRIQPSIHNDNI 1020
Qy      1021  TLEAVVGPQPPSEBPIITHQWSVQMEPPVPCHEYDELERLPAABECALGALFRCPVVRQ 1080
Db      1021  TLEAVVGPQPPSEBPIITHQWSVQMEPPVPCHEYDELERLPAABECALGALFRCPVVRQ 1080
Qy      1087  EILVQVIGTLELVEIBASSMPSLCSLSISFNSKHFHLVGSNSLQVVMKDVVYEX 1087
Db      1087  EILVQVIGTLELVEIBASSMPSLCSLSISFNSKHFHLVGSNSLQVVMKDVVYEX 1087
Qy      1140  EILVQVIGTLELVEIBASSMPSLCSLSISFNSKHFHLVGSNSLQVVMKDVVYEX 1140
Db      1140  EILVQVIGTLELVEIBASSMPSLCSLSISFNSKHFHLVGSNSLQVVMKDVVYEX 1140
Qy      1147  QMLYLYVLSGIGLLILLIFVLVYKGFPRKMLKEMKAGRGVNGIPAEBSQLASGQ 1147
Db      1147  QMLYLYVLSGIGLLILLIFVLVYKGFPRKMLKEMKAGRGVNGIPAEBSQLASGQ 1147

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Db      1141  QMLYLYVLSGIGLLILLIFVLVYKGFPRKMLKEMKAGRGVNGIPAEBSQLASGQ 1200
Qy      1148  EAGDPGLKPLHEKDSGGGKD 1170
Db      1201  EAGDPGLKPLHEKDSGGGKD 1223

RESULT 10
US-10-408-765A-295
; Sequence 295, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408.765A
; NUMBER OF FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 1223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-295

Query Match      99.1%; Score 6053.5; DB 16; Length 1223;
Beet Local Similarity 95.5%; Pred. No. 0;
Matches 1168; Conservative 0; Mismatches 2; Indels 53; Gaps 1;

Qy      1  MKOSCTVMMAMALSGFFPAPASSYNLDVGARSFSPRAGRHFGYRLVQVNGVIVGA 60
Db      1  MKOSCTVMMAMALSGFFPAPASSYNLDVGARSFSPRAGRHFGYRLVQVNGVIVGA 60
Qy      61  PGEKNSGSLYOCOSGTHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Db      61  PGEKNSGSLYOCOSGTHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Qy      121  QNTYLSGICYLFRONLQGRPGROECIKGNVDLVFLPDGSMLOPDEFQKILDFMK 180
Db      121  QNTYLSGICYLFRONLQGRPGROECIKGNVDLVFLPDGSMLOPDEFQKILDFMK 180
Qy      181  DVMKLSNTSYQFAAVQSTSYKTEFPDSYVKRDPALLKHYKHMILLNTFGAINVY 240
Db      181  DVMKLSNTSYQFAAVQSTSYKTEFPDSYVKRDPALLKHYKHMILLNTFGAINVY 240
Qy      241  ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIKHFQTKESQETLH 300
Db      241  ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIKHFQTKESQETLH 300
Qy      301  KPASKPASEPVKIIDTEBEKLDLFTLEOKKIYVIEGTSKODLTSNNMELSSSGISADLSR 360
Db      301  KPASKPASEPVKIIDTEBEKLDLFTLEOKKIYVIEGTSKODLTSNNMELSSSGISADLSR 360
Qy      361  GHAVVAVGAKDMAGGFLDKADLQDDTFIGNEBLTPBEVAGYLGIVTWMPSROKTSIL 420
Db      361  GHAVVAVGAKDMAGGFLDKADLQDDTFIGNEBLTPBEVAGYLGIVTWMPSROKTSIL 420
Qy      421  ASGAPRYOHMGRVILLFQEPQGGHWSQVQTHGTQISYFGGELCGVDVDDGETELLII 480
Db      421  ASGAPRYOHMGRVILLFQEPQGGHWSQVQTHGTQISYFGGELCGVDVDDGETELLII 480
Qy      481  GAPLFYGBORGGRVFIYORROLGFEVESELODPPYLGIRGEGALTALTDINGGLVDA 540
Db      481  GAPLFYGBORGGRVFIYORROLGFEVESELODPPYLGIRGEGALTALTDINGGLVDA 540
Qy      541  VGAPLEBOGAVYIFNGRHGGLSPQSPQRIEQTQVLSGIQWFGRSIHGVKLEGDGLADVA 600

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Db      541 VGAPLEBEGAVYIFNGRHGGLSPQSPQRIEGTVLSGIQMRGRSHGVKDLGEGDLAVYA 600
Qy      601 VGASQMTVLSSRPVDMVMTLMSFSPAPAI PVHEVECSYSTSNKKEGVNITTCFOIKSLY 660
Db      601 VGASQMTVLSSRPVDMVMTLMSFSPAPAI PVHEVECSYSTSNKKEGVNITTCFOIKSLI 660
Qy      661 POFQGRLVANLTYTLQDGHRTTRRGGLPPGGRHRLRNIAVTTSMSCDTSFHFPPVCQD 720
Db      661 POFQGRLVANLTYTLQDGHRTTRRGGLPPGGRHRLRNIAVTTSMSCDTSFHFPPVCQD 720
Qy      721 LISPIVNSLNFSLMEEGTTPDQRAQKDIPIILRPSLSHSTWELPEKNGCEBKKECAN 780
Db      721 LISPIVNSLNFSLMEEGTTPDQRAQKDIPIILRPSLSHSTWELPEKNGCEBKKECAN 780
Qy      781 LRVSPSPARSRLRLTAFAASLSVELSLNLEEDAYWQDLHFPGLSPFRKVEMLKPHSQ 840
Db      781 LRVSPSPARSRLRLTAFAASLSVELSLNLEEDAYWQDLHFPGLSPFRKVEMLKPHSQ 840
Qy      841 IPVSCSELPEBSRLLSRALSCNVSSPIFKAGSHVALQMMFTLVNNSWGDVVELHANVTC 900
Db      841 IPVSCSELPEBSRLLSRALSCNVSSPIFKAGSHVALQMMFTLVNNSWGDVVELHANVTC 900
Qy      901 NNEDSDLEDNSATTIIPILYPINILIQDOEDSTLYVSTFKPKIKHQVKMYO----- 954
Db      901 NNEDSDLEDNSATTIIPILYPINILIQDOEDSTLYVSTFKPKIKHQVKMYO----- 954
Qy      955 -----VRIPSIDHNIP 967
Db      955 -----VRIPSIDHNIP 967
Qy      961 EMQSKQILCRPAGDAEHTVGAQEGELPCPMGVSBAFRDNI RAGCVRRIQPSIDHNIP 1020
Db      961 EMQSKQILCRPAGDAEHTVGAQEGELPCPMGVSBAFRDNI RAGCVRRIQPSIDHNIP 1020
Qy      968 TLEAVGVPPQPSSEPTTHQMSVQMEPPVCHYEDELRLPDAEPCLPQALFRCPVFRQ 1027
Db      968 TLEAVGVPPQPSSEPTTHQMSVQMEPPVCHYEDELRLPDAEPCLPQALFRCPVFRQ 1027
Qy      1021 TLEAVGVPPQPSSEPTTHQMSVQMEPPVCHYEDELRLPDAEPCLPQALFRCPVFRQ 1080
Db      1021 TLEAVGVPPQPSSEPTTHQMSVQMEPPVCHYEDELRLPDAEPCLPQALFRCPVFRQ 1080
Qy      1028 ELIVOVITLLEVEIEASMSPLCSSISFNSSKHHLVGSNLSLAQVMKDVVYEX 1087
Db      1028 ELIVOVITLLEVEIEASMSPLCSSISFNSSKHHLVGSNLSLAQVMKDVVYEX 1087
Qy      1081 ELIVOVITLLEVEIEASMSPLCSSISFNSSKHHLVGSNLSLAQVMKDVVYEX 1140
Db      1081 ELIVOVITLLEVEIEASMSPLCSSISFNSSKHHLVGSNLSLAQVMKDVVYEX 1140
Qy      1088 QMLVLYVLSGIGGLLLLLIPIVLYKVGPFKKNLEKMKAGRGVNGI PAEDSEQLASQ 1147
Db      1141 QMLVLYVLSGIGGLLLLLIPIVLYKVGPFKKNLEKMKAGRGVNGI PAEDSEQLASQ 1200
Qy      1148 EAQDPGCLKPLHEKDSGSGKMD 1170
Db      1201 EAQDPGCLKPLHEKDSGSGKMD 1223

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## RESULT 11

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US-10-473-127-1736
; Sequence 1736, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zydos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1736

```

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; LENGTH: 1223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1736
Query Match      99.1%; Score 6053.5; DB 16; Length 1223;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 1168; Conservative 0; Mismatches 2; Indels 53; Gaps 1;
Qy      1 MKDSCTVMAALLSGFFFPAPASSYNLDVNGARSPFPAGRHFGYRVLOVNGVTVGA 60
Db      1 MKDSCTVMAALLSGFFFPAPASSYNLDVNGARSPFPAGRHFGYRVLOVNGVTVGA 60
Qy      61 PGENSGTSLYQCCSGTGHCIPVTLRGSNTSKTLGNTLATDPDGSGLACDPGLSRCD 120
Db      61 PGENSGTSLYQCCSGTGHCIPVTLRGSNTSKTLGNTLATDPDGSGLACDPGLSRCD 120
Qy      121 QNTYLSGLCYLFRONLQPMLOGRPGFOECI KGNVNDLVFLPDGSMISLOPDEFOKILDPMK 180
Db      121 QNTYLSGLCYLFRONLQPMLOGRPGFOECI KGNVNDLVFLPDGSMISLOPDEFOKILDPMK 180
Qy      181 DVMKLSNTSYQFAAVQFSTSYKTEPDSYVKKRDPDALIKHYKMLLTNTEGAINVY 240
Db      181 DVMKLSNTSYQFAAVQFSTSYKTEPDSYVKKRDPDALIKHYKMLLTNTEGAINVY 240
Qy      241 ATEVFRBELGARPATVYLIIITDGEATDSCNIDAADIIRYIIIGIKHPOTKESQETLH 300
Db      241 ATEVFRBELGARPATVYLIIITDGEATDSCNIDAADIIRYIIIGIKHPOTKESQETLH 300
Qy      301 KFAKSPASEFVKILDTBEKLDLFTLEOKKIYVEGTSKODLSFNNELSSGISAQLSR 360
Db      301 KFAKSPASEFVKILDTBEKLDLFTLEOKKIYVEGTSKODLSFNNELSSGISAQLSR 360
Qy      361 GHAVAVGAGADWAGCEFLDKADLODDPTIGNEBLTEVEBAGVLYGTWTMLPSRQKTSIL 420
Db      361 GHAVAVGAGADWAGCEFLDKADLODDPTIGNEBLTEVEBAGVLYGTWTMLPSRQKTSIL 420
Qy      421 ASGAPRYOHMGVRLLEPQEGGHWMSOVQTIHGTQISYFGELGCVDDVDGTELLLI 480
Db      421 ASGAPRYOHMGVRLLEPQEGGHWMSOVQTIHGTQISYFGELGCVDDVDGTELLLI 480
Qy      481 GAPIFYBQGRGVFIYORROLGFEVESELOGDGYLGRGEXALTLDINSGGLDVYA 540
Db      481 GAPIFYBQGRGVFIYORROLGFEVESELOGDGYLGRGEXALTLDINSGGLDVYA 540
Qy      541 VGAPLEBEGAVYIFNGRHGGLSPQSPQRIEGTVLSGIQMRGRSHGVKDLGEGDLAVYA 600
Db      541 VGAPLEBEGAVYIFNGRHGGLSPQSPQRIEGTVLSGIQMRGRSHGVKDLGEGDLAVYA 600
Qy      601 VGASQMTVLSSRPVDMVMTLMSFSPAPAI PVHEVECSYSTSNKKEGVNITTCFOIKSLY 660
Db      601 VGASQMTVLSSRPVDMVMTLMSFSPAPAI PVHEVECSYSTSNKKEGVNITTCFOIKSLI 660
Qy      661 POFQGRLVANLTYTLQDGHRTTRRGGLPPGGRHRLRNIAVTTSMSCDTSFHFPPVCQD 720
Db      661 POFQGRLVANLTYTLQDGHRTTRRGGLPPGGRHRLRNIAVTTSMSCDTSFHFPPVCQD 720
Qy      721 LISPIVNSLNFSLMEEGTTPDQRAQKDIPIILRPSLSHSTWELPEKNGCEBKKECAN 780
Db      721 LISPIVNSLNFSLMEEGTTPDQRAQKDIPIILRPSLSHSTWELPEKNGCEBKKECAN 780
Qy      781 LRVSPSPARSRLRLTAFAASLSVELSLNLEEDAYWQDLHFPGLSPFRKVEMLKPHSQ 840
Db      781 LRVSPSPARSRLRLTAFAASLSVELSLNLEEDAYWQDLHFPGLSPFRKVEMLKPHSQ 840
Qy      841 IPVSCSELPEBSRLLSRALSCNVSSPIFKAGSHVALQMMFTLVNNSWGDVVELHANVTC 900
Db      841 IPVSCSELPEBSRLLSRALSCNVSSPIFKAGSHVALQMMFTLVNNSWGDVVELHANVTC 900
Qy      901 NNEDSDLEDNSATTIIPILYPINILIQDOEDSTLYVSTFKPKIKHQVKMYO----- 954
Db      901 NNEDSDLEDNSATTIIPILYPINILIQDOEDSTLYVSTFKPKIKHQVKMYO----- 954

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Qy 955 -----VRIQPSIHDP 967  
Db 961 EMQTSKQILCRPAGDAHEHTVGAQEGELPCPMGVSEAPRDNIRAGPCRVRIQPSIHDP 1020  
Qy 968 TLEAVVGPQPPSEBPTTHQMSVQMEPPVPCHELELELPDAEPCLPALFRCPVVRQ 1027  
Db 1021 TLEAVVGPQPPSEBPTTHQMSVQMEPPVPCHELELELPDAEPCLPALFRCPVVRQ 1080  
Qy 1028 EILVQVITLLEVGEIEASMSFSLCSSISFNSSKHHLVGSNLSLAQVVMKDVVYK 1087  
Db 1081 EILVQVITLLEVGEIEASMSFSLCSSISFNSSKHHLVGSNLSLAQVVMKDVVYK 1140  
Qy 1088 QMLYLYVLSIGIGLLLLLLIFLYVYKVPFRKMLKEKMEAGRGVNGIPAEBSQASGQ 1147  
Db 1141 QMLYLYVLSIGIGLLLLLLIFLYVYKVPFRKMLKEKMEAGRGVNGIPAEBSQASGQ 1200  
Qy 1148 EAGDPGCLKPLHEKXSESGGKD 1170  
Db 1201 EAGDPGCLKPLHEKXSESGGKD 1223

## RESULT 12

US-10-872-198-130  
; Sequence 130, Application US/10872198  
; Publication No. US20050002897A1  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich HAUPTS  
; APPLICANT: Andre KOLTERMANN  
; APPLICANT: Christiaan VOETSMETIER  
; APPLICANT: Ulrich Ketting  
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF  
; FILE REFERENCE: 04156.0002U4  
; CURRENT APPLICATION NUMBER: US/10/872,198  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 60/543,518  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/524,960  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: EP 04003058  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: EP 03025871  
; PRIOR FILING DATE: 2003-11-11  
; PRIOR APPLICATION NUMBER: EP 03025851  
; PRIOR FILING DATE: 2003-11-10  
; PRIOR APPLICATION NUMBER: EP 03013819  
; PRIOR FILING DATE: 2003-06-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 130  
; LENGTH: 1145  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-872-198-130

Query Match 98.0%; Score 5981; DB 17; Length 1145;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 YNLDVRGARSPSPRAGHFGYRVLOVANGVIVGAPGSGNSTGSIYQCSGTGHCPLPYTL 85  
Db 1 YNLDVRGARSPSPRAGHFGYRVLOVANGVIVGAPGSGNSTGSIYQCSGTGHCPLPYTL 60  
Qy 86 RGSNTSXYLGMTLATDPTDGSILACDPGLSRTCDQNTYLSGLCYLFRONTLQGPWLQGRP 145  
Db 61 RGSNTSXYLGMTLATDPTDGSILACDPGLSRTCDQNTYLSGLCYLFRONTLQGPWLQGRP 120  
Qy 146 GFQECIKGNVDLVFLFDGSMSLQDPDEFOKILDFMKDVWKKLSNTSYQPAAVOFSTSYKTE 205  
Db 121 GFQECIKGNVDLVFLFDGSMSLQDPDEFOKILDFMKDVWKKLSNTSYQPAAVOFSTSYKTE 180  
Qy 206 FDFSDYVRKQPDALLKHVKMELLTNTFGAINVATEVFRBELGARDPATKVLIIITDG 265  
Db 206 FDFSDYVRKQPDALLKHVKMELLTNTFGAINVATEVFRBELGARDPATKVLIIITDG 265

Db 181 FDFSDYVRKQPDALLKHVKMELLTNTFGAINVATEVFRBELGARDPATKVLIIITDG 240  
Qy 266 EATSGNIDAKODIRYIIGIKGHFOTKESQETLHKRASPAPSPVYILDTPEKLDLFT 325  
Db 241 EATSGNIDAKODIRYIIGIKGHFOTKESQETLHKRASPAPSPVYILDTPEKLDLFT 300  
Qy 326 ELQKKIVIBGTSKODLTSFNMELSSSGISADLSRGAHVAVGAKDMAGFLDLKADLQ 385  
Db 301 ELQKKIVIBGTSKODLTSFNMELSSSGISADLSRGAHVAVGAKDMAGFLDLKADLQ 360  
Qy 386 DDTFIGNEPILTEPRAGYLYTWTWPLSRQKTSILASGARRYQMGVLLPOEQGGGW 445  
Db 361 DDTFIGNEPILTEPRAGYLYTWTWPLSRQKTSILASGARRYQMGVLLPOEQGGGW 420  
Qy 446 SQVOTIHGTOIGSPFGEELGVDDQGETELLIGAPLYPYGEORGRVPIYORRQGF 505  
Db 421 SQVOTIHGTOIGSPFGEELGVDDQGETELLIGAPLYPYGEORGRVPIYORRQGF 480  
Qy 506 EVSELQDPCYPLGRFGEAITTALTDINGDLVDVAVGAPLEBQAVYIFNGRHGGLSP 565  
Db 481 EVSELQDPCYPLGRFGEAITTALTDINGDLVDVAVGAPLEBQAVYIFNGRHGGLSP 540  
Qy 566 SQRIEGTQVLSGIOWFGRSIGHVYKDLBGDLADVAVGAEQMTVLSRPVDMVTLMSFS 625  
Db 541 SQRIEGTQVLSGIOWFGRSIGHVYKDLBGDLADVAVGAEQMTVLSRPVDMVTLMSFS 600  
Qy 626 PABIPVHEVCSTYSNKKMEGVNITICFOIKSLYPOFOGRVLANLYTTLQDGHRTRR 685  
Db 601 PABIPVHEVCSTYSNKKMEGVNITICFOIKSLYPOFOGRVLANLYTTLQDGHRTRR 660  
Qy 686 GLPFGHHELRNIAVTTSMSCDTFSFHPVYQVDLISPINVSINFLSMBEETPRDQRA 745  
Db 661 GLPFGHHELRNIAVTTSMSCDTFSFHPVYQVDLISPINVSINFLSMBEETPRDQRA 720  
Qy 746 QGKDIPTILRPSLSHSEWETIPREKNCGBDKCEANLAVSSPARSLRLTAPASLSVEL 805  
Db 721 QGKDIPTILRPSLSHSEWETIPREKNCGBDKCEANLAVSSPARSLRLTAPASLSVEL 780  
Qy 806 SLNLSBEDAYWQDLHFPPLGLSPFRKYMELKPHSQIPVSCBELPEBSRLSRLASCNVSS 865  
Db 781 SLNLSBEDAYWQDLHFPPLGLSPFRKYMELKPHSQIPVSCBELPEBSRLSRLASCNVSS 840  
Qy 866 PIFRAGHSVALQWMTLVNVSWSGDSVELHANVTCCNNEBDLLEDSATTTIPLYPINI 925  
Db 841 PIFRAGHSVALQWMTLVNVSWSGDSVELHANVTCCNNEBDLLEDSATTTIPLYPINI 900  
Qy 926 LIQDQEDSTLYVSTTPKGPXIHQVKMYQVRIQPSIHDPNIPITLEAVVGPQPPSEBPT 985  
Db 901 LIQDQEDSTLYVSTTPKGPXIHQVKMYQVRIQPSIHDPNIPITLEAVVGPQPPSEBPT 960  
Qy 986 HQMSVQMEPPVPCHELELELPDAEPCLPALFRCPVVRQELIVQITLLEVGEIEA 1045  
Db 961 HQMSVQMEPPVPCHELELELPDAEPCLPALFRCPVVRQELIVQITLLEVGEIEA 1020  
Qy 1046 SSMFSLCSSISFNSSKHHLVGSNLSLAQVVMKDVVYKQMLYLYVLSIGIGLLLL 1105  
Db 1021 SSMFSLCSSISFNSSKHHLVGSNLSLAQVVMKDVVYKQMLYLYVLSIGIGLLLL 1080  
Qy 1106 LIPIVLYVYKVPFRKMLKEKMEAGRGVNGIPAEBSQASGQAGDPGCLKPLHEKXSES 1165  
Db 1081 LIPIVLYVYKVPFRKMLKEKMEAGRGVNGIPAEBSQASGQAGDPGCLKPLHEKXSES 1140  
Qy 1166 GGGKD 1170  
Db 1141 GGGKD 1145

## RESULT 13

US-11-021-951-130  
; Sequence 130, Application US/11021951  
; Publication No. US20050175581A1  
; GENERAL INFORMATION:  
; APPLICANT: HAUPTS, Ulrich

APPLICANT: KOLTERMANN, Andre  
APPLICANT: SCHEIDIG, Andreas  
APPLICANT: VOTSMEIER, Christian  
APPLICANT: Ketting, Ulrich  
APPLICANT: COCO, Wayne Michael  
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical  
FILE REFERENCE: 04156.0002U5  
CURRENT APPLICATION NUMBER: US/11/021,951  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: 10/872,198  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 60/543,518  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/524,960  
PRIOR FILING DATE: 2003-11-25  
PRIOR APPLICATION NUMBER: EP 04003058  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: EP 03025871  
PRIOR FILING DATE: 2003-11-11  
PRIOR APPLICATION NUMBER: EP 03025851  
PRIOR FILING DATE: 2003-11-10  
PRIOR APPLICATION NUMBER: EP 03013819  
PRIOR FILING DATE: 2003-06-18  
NUMBER OF SEQ ID NOS: 191  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 130  
LENGTH: 1145.  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-021-951-130

Query Match 98.0%; Score 5981; DB 20; Length 1145;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 YNLDVGRGARSFPPRAAGFRGVRVQVNGVVGAPGEGNSGSLYQCGSGTGHCLPTL 85  
DB 1 YNLDVGRGARSFSPRAGRGFRVQVNGVVGAPGEGNSGSLYQCGSGTGHCLPTL 60  
QY 86 RGSNTSKLGMTLATDPTDGSLLACDPGLSRTCDONTLSGLCYLFRONTLQGPMLQGRP 145  
DB 61 RGSNTSKLGMTLATDPTDGSLLACDPGLSRTCDONTLSGLCYLFRONTLQGPMLQGRP 120  
QY 146 GFQECIKGNVDVFLFDGSGMSLQPDFOKILDFMKDVVKLSNTSYQFAAVQFSTSYKTE 205  
DB 121 GFQECIKGNVDVFLFDGSGMSLQPDFOKILDFMKDVVKLSNTSYQFAAVQFSTSYKTE 180  
QY 206 PFFSDYVRKRDPAKDLKHYKEMLLTNTFGAINVVADEVFREELGARPDATVLLIITDG 265  
DB 181 PFFSDYVRKRDPAKDLKHYKEMLLTNTFGAINVVADEVFREELGARPDATVLLIITDG 240  
QY 266 EATDGNIDAAKOIIRYIIGIKGHQTKESQETLHKFKSPKSEPVKILDTPEKLDKDTFT 325  
DB 241 EATDGNIDAAKOIIRYIIGIKGHQTKESQETLHKFKSPKSEPVKILDTPEKLDKDTFT 300  
QY 326 ELQKKIYVLEGTSKDILTSFNNELSSSGISADLSRGHAAVGAADKMAAGFLDKADQ 385  
DB 301 ELQKKIYVLEGTSKDILTSFNNELSSSGISADLSRGHAAVGAADKMAAGFLDKADQ 360  
QY 386 DDTFGNEPLTPEVRAGVYGYVTVMPSRQKTSLLASGAPRYQHMGRVLLFQEPQGGHW 445  
DB 361 DDTFGNEPLTPEVRAGVYGYVTVMPSRQKTSLLASGAPRYQHMGRVLLFQEPQGGHW 420  
QY 446 SOVOTIHGQISYFSGELCGVDVDDGETELLIGAPLFYEGORSGRVITYOROLGPE 505  
DB 421 SOVOTIHGQISYFSGELCGVDVDDGETELLIGAPLFYEGORSGRVITYOROLGPE 480  
QY 506 EYSELQGDGPGYPLRGGAITALTJINGDGLVDVAVGABLEQGAVYIFNGHGGSLSP 565  
DB 481 EYSELQGDGPGYPLRGGAITALTJINGDGLVDVAVGABLEQGAVYIFNGHGGSLSP 540  
QY 566 SQRIGTQVLSGIQMFGRSHGVKLEGLADVAVGAESQMTVLSSRPVDMVTLMSPS 625

DB 541 SQRIGTQVLSGIQMFGRSHGVKLEGLADVAVGAESQMTVLSSRPVDMVTLMSPS 600  
QY 626 PAEIPVHEVECSYSTSNKKEGVNITTCFOIKSLYPOFQGLVANLTYTLOLDGRTTTR 685  
DB 601 PAEIPVHEVECSYSTSNKKEGVNITTCFOIKSLYPOFQGLVANLTYTLOLDGRTTTR 660  
QY 686 GLPFGGRHELRNNAVTTSNCTDPSFHPVQVODLSPINVSINFSIMEEGTPRODRA 745  
DB 661 GLPFGGRHELRNNAVTTSNCTDPSFHPVQVODLSPINVSINFSIMEEGTPRODRA 720  
QY 746 QGKDIPLRLSLHSETWEIPFEKNCGEDKCEANLRVSPASRALRTAFASLSEVL 805  
DB 721 QGKDIPLRLSLHSETWEIPFEKNCGEDKCEANLRVSPASRALRTAFASLSEVL 780  
QY 806 SLNLSEDAVYVQDLHPPGLSFRKYMELKPHSQIIPVSCLELPEESRLSRALSCNVSS 865  
DB 781 SLNLSEDAVYVQDLHPPGLSFRKYMELKPHSQIIPVSCLELPEESRLSRALSCNVSS 840  
QY 866 PIFRAGHVALQMMNTLVNSKGDVSLHANVTCNNEDSLLDENSATTTIPIIYPINI 925  
DB 841 PIFRAGHVALQMMNTLVNSKGDVSLHANVTCNNEDSLLDENSATTTIPIIYPINI 900  
QY 926 LIQDQEDSTLYVSTFKGPKIHQVKNVQVRIOPSIDHNTPTLEAVVGVQPPSEGPIT 985  
DB 901 LIQDQEDSTLYVSTFKGPKIHQVKNVQVRIOPSIDHNTPTLEAVVGVQPPSEGPIT 960  
QY 986 HQMSVQMPVPVCHYEDLERLPDAEPCLPGALFRCPVFRQELIVQYIGTLEVGELTA 1045  
DB 961 HQMSVQMPVPVCHYEDLERLPDAEPCLPGALFRCPVFRQELIVQYIGTLEVGELTA 1020  
QY 1046 SSMFSLCSLSISFNSSGHFHLVGSNMSLAQVNVKVDVVEKQMLYVLVSGIGLLILL 1105  
DB 1021 SSMFSLCSLSISFNSSGHFHLVGSNMSLAQVNVKVDVVEKQMLYVLVSGIGLLILL 1080  
QY 1106 LIFIVLYVGFPPKNTLKKEMAGRGVPGIQAEDSEQLASQEAQDPGCLPLHKQSES 1165  
DB 1081 LIFIVLYVGFPPKNTLKKEMAGRGVPGIQAEDSEQLASQEAQDPGCLPLHKQSES 1140  
QY 1166 GGGKD 1170  
DB 1141 GGGKD 1145  
RESULT 14  
US-10-473-1738  
; Sequence 1738, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1738  
; LENGTH: 1145  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1738

Query Match 97.8%; Score 5973; DB 16; length 1145;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 26 YNLVDRGARSPSPAGAHFGYRVLVQVNGVTVGAPGREGNSTGSLYQCGSTGHCPLPTL 85
DB 1 YNLVDRGARSPSPAGAHFGYRVLVQVNGVTVGAPGREGNSTGSLYQCGSTGHCPLPTL 60
QY 86 RGSNTSKYLGMWLTATDPTDGSIIACDPGLSRTCPQNTYLSGLCYLFPQNTLQGPMLQGRP 145
DB 61 RGSNTSKYLGMWLTATDPTDGSIIACDPGLSRTCPQNTYLSGLCYLFPQNTLQGPMLQGRP 120
QY 146 GFOECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMDVWKKLSNTSYQFAVQFSTYKTE 205
DB 121 GFOECIKGNVDLVFLFDGSMSLQDPDEFQKILDFMDVWKKLSNTSYQFAVQFSTYKTE 180
QY 206 PDFSTYVYKRPDALLKIVKMLLTNTFGAINVYATVFEELGARDATKVLIIITDG 265
DB 181 PDFSTYVYKRPDALLKIVKMLLTNTFGAINVYATVFEELGARDATKVLIIITDG 240
QY 266 EATDSGNIDAAKDIIRYIIGIKHQTESOETLHKFASKPASEPVKILDTPEKIKDLFT 325
DB 241 EATDSGNIDAAKDIIRYIIGIKHQTESOETLHKFASKPASEPVKILDTPEKIKDLFT 300
QY 326 ELQKKIYIEGTSKODLTSFNMELSSSGISADLSRGHAVGAVGAKDWAAGFLDLKADLQ 385
DB 301 ELQKKIYIEGTSKODLTSFNMELSSSGISADLSRGHAVGAVGAKDWAAGFLDLKADLQ 360
QY 386 DDTFIGNEPILPEVYAGYLGITVTVLBSRQKTSLSASGAPRYOHMGVLLFOEPQGGGHW 445
DB 361 DDTFIGNEPILPEVYAGYLGITVTVLBSRQKTSLSASGAPRYOHMGVLLFOEPQGGGHW 420
QY 446 SOVQTHGTQIGSYGGELCGVDVQDDETELLIIGALFLYGEORGSGVFIYQORQIGFE 505
DB 421 SOVQTHGTQIGSYGGELCGVDVQDDETELLIIGALFLYGEORGSGVFIYQORQIGFE 480
QY 506 EVSBLQDGPYPLGFGFEGAITALTINDGLADVAVGAPLEBOGAVYIFNGRHGGLSPQ 565
DB 481 EVSBLQDGPYPLGFGFEGAITALTINDGLADVAVGAPLEBOGAVYIFNGRHGGLSPQ 540
QY 566 SORFEGTOVLSGIGFGRSHGVKDLBEDGLADVAVGAESQMTIVLSPRVVDMVTLMSFS 625
DB 541 SORFEGTOVLSGIGFGRSHGVKDLBEDGLADVAVGAESQMTIVLSPRVVDMVTLMSFS 600
QY 626 PABIPVHEVGSYSNMGKEGVNTTCFOIKSLYPOQGRVAVLTATTLQDGHRTRR 685
DB 601 PABIPVHEVGSYSNMGKEGVNTTCFOIKSLYPOQGRVAVLTATTLQDGHRTRR 660
QY 686 GLFVGRHELARNIAVTTSMSCDTPSFHFPVCVODLISPIVNSLNFSLMBEETPRDQRA 745
DB 661 GLFVGRHELARNIAVTTSMSCDTPSFHFPVCVODLISPIVNSLNFSLMBEETPRDQRA 720
QY 746 QGKQPIPLRPSLHSETWIDPEKXGGEKXCEANLRVFSFSPARSARALTAFASLSVEL 805
DB 721 QGKQPIPLRPSLHSETWIDPEKXGGEKXCEANLRVFSFSPARSARALTAFASLSVEL 780
QY 806 SLSTLBERAVVVOJDLHFRPGLSRKXVEMLKPHSGIIPISCEELPBESLISRALSCVNS 865
DB 781 SLSTLBERAVVVOJDLHFRPGLSRKXVEMLKPHSGIIPISCEELPBESLISRALSCVNS 840
QY 866 PIFKAGSHVALQMMFNTLVNSMGDSVELHANVTCNNDSDLLEDNSATIIIPILYPINI 925
DB 841 PIFKAGSHVALQMMFNTLVNSMGDSVELHANVTCNNDSDLLEDNSATIIIPILYPINI 900
QY 926 LIQDQDSTLYVSTPKGPKIHQVKNYQVRIQPSIHDAIPTLEAVVGVQPSSEGIT 985
DB 901 LIQDQDSTLYVSTPKGPKIHQVKNYQVRIQPSIHDAIPTLEAVVGVQPSSEGIT 960
QY 986 HGVNVQMPVPVCHYEDLERLPDAABPCLRGALFRCPVFRQELIYQYIGTLELVGEREA 1045
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QY 1046 SSMFSLCSLSISFNSKHFHLVGSNASLQVWVKVDVVEKQMLYLYVLSGIGLLLL 1105
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QY 1106 LIFIVLYKVGFPKRLNKKKMBAGRGVNGGIPADDSQSLASGQADPGCLKPLHKSES 1165
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## RESULT 15

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US-10-473-127-1741
; Sequence 1741, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1741
; LENGTH: 1086
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-473-127-1741

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QY 61 PGBGNSYGSLYQCGSTGHCPLPTLKGSTNTSKYLGMWLTATDPTDGSIIACDPGLSRTCD 120
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QY 121 QNTYLSGLCYLFPQNTLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFPMK 180
DB 121 QNTYLSGLCYLFPQNTLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDEFQKILDFPMK 180
QY 181 DVWKKLSNTSYQFAVQFSTYKTEPDFSDYVYKRPDALLKIVKMLLTNTFGAINVY 240
DB 181 DVWKKLSNTSYQFAVQFSTYKTEPDFSDYVYKRPDALLKIVKMLLTNTFGAINVY 240
QY 241 ATEVFEELGARDATKVLIIITDGEATDSGNIDAAKDIIRYIIGIKHQTESOETLH 300
DB 241 ATEVFEELGARDATKVLIIITDGEATDSGNIDAAKDIIRYIIGIKHQTESOETLH 300
QY 301 KPASKPASEPVKILDTPEKIKDLFTELOKKIYIEGTSKODLTSFNMELSSSGISADLSR 360
DB 301 KPASKPASEPVKILDTPEKIKDLFTELOKKIYIEGTSKODLTSFNMELSSSGISADLSR 360
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Db 421 ASGARPYOMGRVLLFQEPQGGGHSQVQTIHGTOIGSYFGGELCGVVDQDGETELLII 480
QY 481 GAPLFYGEORGRVFIYQRRQLGFEEVSELODPCGYLGRFGEAITALTIDINGDLADVA 540
Db 481 GAPLFYGEORGRVFIYQRRQLGFEEVSELODPCGYLGRFGEAITALTIDINGDLADVA 540
QY 541 VGAPLEBQAVYIFNGRHGGLSPQSORLEGTVLSGIQWFGRSIHGVKDLEGDGLADVA 600
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QY 601 VCAESQMTVLSRPPVDMYTLMSFSPAEPVHEVCSYSTSNKKEGVNITTCFOIKSLY 660
Db 601 VCAESQMTVLSRPPVDMYTLMSFSPAEPVHEVCSYSTSNKKEGVNITTCFOIKSLY 660
QY 661 POFQRLVANLTYTLOLDGHTRRRGLFPGGRHELRRNIAVTTSMSCDFFSFPVCVOD 720
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Db 960 IHDHNIPTLEAVGVPOPPSEGPITHQWSVOMEPPVPCHYEDLERLPDAEPCLPALFR 1019
QY 1021 CPVVRQELVQVIGTLELVGEIEASSMPSLCCSSISFNSSKHFLYGSNASTLAQVVMK 1080
Db 1020 CPVVRQELVQVIGTLELVGEIEASSMPSLCCSSISFNSSKHFLYGSNASTLAQVVMK 1079
QY 1081 VDVVYEX 1087
Db 1080 VDVVYEX 1086
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Job time : 184 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2005, 19:20:14 ; Search time 483 Seconds

(without alignments)  
2829.332 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 1 MKDSCITVMMALLSGFFFF.....DPGLKPLHEKDSGGGKD 1170

Sequence:

BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6106	100.0	1170	1 PCT-US02-09671-1743	Sequence 1743, Ap
2	6106	100.0	1170	22 US-09-791-537-83469	Sequence 83469, A
3	6106	100.0	1170	24 US-09-945-265-2	Sequence 2, Appl1
4	6106	100.0	1170	30 US-10-473-127-1743	Sequence 1743, Ap
5	6098	99.9	1170	1 PCT-US02-09671-1737	Sequence 1737, Ap
6	6098	99.9	1170	1 PCT-US02-09671-1739	Sequence 1739, Ap
7	6098	99.9	1170	1 PCT-US02-09671-1742	Sequence 1742, Ap
8	6098	99.9	1170	1 PCT-US03-12946-3007	Sequence 3007, Ap
9	6098	99.9	1170	1 PCT-US03-40978-1088	Sequence 1088, Ap
10	6098	99.9	1170	19 US-09-592-617A-42	Sequence 42, Appl
11	6098	99.9	1170	19 US-09-592-617C-42	Sequence 42, Appl
12	6098	99.9	1170	22 US-09-791-537-118794	Sequence 118794, A
13	6098	99.9	1170	27 US-10-170-2058-35754	Sequence 35754, A
14	6098	99.9	1170	28 US-10-261-164-1	Sequence 1, Appl1
15	6098	99.9	1170	29 US-10-325-899-9350	Sequence 9350, Ap
16	6098	99.9	1170	30 US-10-473-127-1737	Sequence 1737, Ap
17	6098	99.9	1170	30 US-10-473-127-1739	Sequence 1739, Ap
18	6098	99.9	1170	30 US-10-473-127-1742	Sequence 1742, Ap
19	6098	99.9	1170	33 US-10-741-600-1088	Sequence 1088, Ap
20	6098	99.9	1170	34 US-10-802-508-42	Sequence 42, Appl
21	6098	99.9	1170	36 US-11-000-473-42	Sequence 42, Appl
22	6098	99.9	1170	37 US-60-453-050-11104	Sequence 11104, A
23	6098	99.9	1170	37 US-60-453-057-11104	Sequence 11104, A
24	6098	99.9	1170	37 US-60-455-444-5811	Sequence 5811, Ap
25	6098	99.9	1170	37 US-60-465-241-5811	Sequence 5811, Ap
26	6098	99.9	1170	37 US-60-466-412-11104	Sequence 11104, A
27	6098	99.9	1170	37 US-60-474-850-513	Sequence 513, Ap
28	6098	99.9	1170	37 US-60-487-610-1880	Sequence 1880, Ap
29	6098	99.9	1170	37 US-60-548-091-382	Sequence 382, Ap
30	6098	99.9	1170	37 US-60-582-609-1880	Sequence 1880, Ap
31	6061.5	99.3	1223	1 PCT-US03-40978-1086	Sequence 1086, Ap
32	6061.5	99.3	1223	33 US-10-741-600-1086	Sequence 1086, Ap
33	6061.5	99.3	1223	7 US-60-548-091-380	Sequence 380, Ap
34	6058	99.2	1170	7 US-08-380-167-42	Sequence 42, Appl
35	6058	99.2	1170	7 US-08-380-167A-42	Sequence 42, Appl
36	6058	99.2	1170	8 US-08-476-062-42	Sequence 42, Appl
37	6053.5	99.1	1223	1 PCT-US02-09671-1736	Sequence 1736, Ap
38	6053.5	99.1	1223	22 US-09-791-537-124811	Sequence 124811, A
39	6053.5	99.1	1223	30 US-10-408-765-295	Sequence 295, Ap
40	6053.5	99.1	1223	30 US-10-408-765A-295	Sequence 295, Ap
41	6053.5	99.1	1223	30 US-10-473-127-1736	Sequence 1736, Ap
42	6053.5	99.1	1223	37 US-60-389-987-295	Sequence 295, Ap
43	6053.5	99.1	1223	37 US-60-412-418-295	Sequence 295, Ap
44	5981	98.0	1145	34 US-10-872-198-130	Sequence 130, Ap
45	5973	97.8	1145	1 PCT-US02-09671-1738	Sequence 1738, Ap

## ALIGNMENTS

RESULT 1  
PCT-US02-09671-1743  
; Sequence 1743, Application PC/TUS0209671  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: PCT/US02/09671  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/297,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/358,985  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 2041  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO: 1743  
 ; LENGTH: 1170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 PCT-US02-09671-1743

Query Match 100.0%; Score 6106; DB 1; Length 1170;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 GHAVVAVGAKDMAGGFLDLKADLQDDPTFGNEPLTPEVARGYLGTYVTWLPSRQKTSLL 420
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Qy 481 GAFLEFGORGRVFIYQRRQLGFEVESELQGDPEYPLGRFGEALTALTDINGDLVDVA 540
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Qy 901 NNEDSDLLDNSSATTIPIPIYINILIQOEDSTLYVSFTPKGPKIHQVGMTQVRIOPS 960
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RESULT 2
US-09-791-83469
; Sequence 83469, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 83469
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-83469

Query Match 100.0%; Score 6106; DB 22; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  
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QY 721 LISPINVSLNFSLWEEGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGEBKCEAN 780
DB 721 LISPINVSLNFSLWEEGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGEBKCEAN 780
QY 781 LRVSPSPARSRALRLTAPASISVELSNLEBDAYWOLDLHPPGGLSFRVEMLKPHSQ 840
DB 781 LRVSPSPARSRALRLTAPASISVELSNLEBDAYWOLDLHPPGGLSFRVEMLKPHSQ 840
QY 841 IIVSCBELPEBSRLSLRSLSCNVSSPIFKAGSHVALQMFENTLVNSSGDSVELHANVC 900
DB 841 IIVSCBELPEBSRLSLRSLSCNVSSPIFKAGSHVALQMFENTLVNSSGDSVELHANVC 900
QY 901 NNEBSDLLEDNASTTTIPIILYPINILIQDEBISTLYVSFTPKGPKIHQVKMIOVRIOPS 960
DB 901 NNEBSDLLEDNASTTTIPIILYPINILIQDEBISTLYVSFTPKGPKIHQVKMIOVRIOPS 960
QY 961 IHDNIPITLNAVGVPOPPSGPITTHQSVOMEPPVCHYEDLERLDAAPCLPGLALFR 1020
DB 961 IHDNIPITLNAVGVPOPPSGPITTHQSVOMEPPVCHYEDLERLDAAPCLPGLALFR 1020
QY 1021 CPVYPROBILIOVGTLELVEIEIASMSFSCSSISTISFNSSKHRLVGSNASTLAQVVMK 1080
DB 1021 CPVYPROBILIOVGTLELVEIEIASMSFSCSSISTISFNSSKHRLVGSNASTLAQVVMK 1080
QY 1081 VDVIYKQMLVLYLSGIGLILLILIFIVLYKVGFFRNLKEKMEAGRGVPMGIPADS 1140
DB 1081 VDVIYKQMLVLYLSGIGLILLILIFIVLYKVGFFRNLKEKMEAGRGVPMGIPADS 1140
QY 1141 EQLASQGEAGDPGCLKPLHEKDSGSGKD 1170
DB 1141 EQLASQGEAGDPGCLKPLHEKDSGSGKD 1170

```

RESULT 3  
US-09-945-265-2

```

; Sequence 2, Application US/09945265
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimacka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CBN-002CP
; CURRENT APPLICATION NUMBER: US/09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1170
; TYPE: PRT

```

```

i ORGANISM: Homo sapiens
US-09-945-265-2
Query Match 100.0%; Score 6106; DB 24; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSCITVMMALLSGFFFPAPASSYVLDVGAASSPPAPGRVLYOVNGVYVGA 60
DB 1 MKSCITVMMALLSGFFFPAPASSYVLDVGAASSPPAPGRVLYOVNGVYVGA 60
QY 61 PGBNSGSLYQCGSGHGLPVTLRGSNTYSKYIGMTLATDPDGSILACDPGLSTCD 120
DB 61 PGBNSGSLYQCGSGHGLPVTLRGSNTYSKYIGMTLATDPDGSILACDPGLSTCD 120
QY 121 QNTYLSGLCYLFRONTQGPMLQGRPGFOECIKGNVDLVFLPDGMSLQDEFOKILDFMK 180
DB 121 QNTYLSGLCYLFRONTQGPMLQGRPGFOECIKGNVDLVFLPDGMSLQDEFOKILDFMK 180
QY 181 DVMKLSNTSYQFAAVOPSTSYKTEPDSYVYKRDPAALLKHYKMLLTNTGALNV 240
DB 181 DVMKLSNTSYQFAAVOPSTSYKTEPDSYVYKRDPAALLKHYKMLLTNTGALNV 240
QY 241 ATEVFRBELGARPATYKVLIIITDGEATDSNDIAADIIIRYIIGIGHFOTKESQETIH 300
DB 241 ATEVFRBELGARPATYKVLIIITDGEATDSNDIAADIIIRYIIGIGHFOTKESQETIH 300
QY 301 KFAKAPSEBFYKIDTFEKLKDLFTLEOKKIYIEGTSKODLTSFNNELSSSGISADLSR 360
DB 301 KFAKAPSEBFYKIDTFEKLKDLFTLEOKKIYIEGTSKODLTSFNNELSSSGISADLSR 360
QY 361 GHAVVAGVAKDWAAGFLDKADLQDDTFIGNEBLPEVBAQYGYVTWLPSSQKTSLL 420
DB 361 GHAVVAGVAKDWAAGFLDKADLQDDTFIGNEBLPEVBAQYGYVTWLPSSQKTSLL 420
QY 421 ASGAPRYOHMGRVLLFOBPQGGHMSQVOTIHGQISYFGGELCGVVDODGETELLII 480
DB 421 ASGAPRYOHMGRVLLFOBPQGGHMSQVOTIHGQISYFGGELCGVVDODGETELLII 480
QY 481 GAPLFYEGORGRVFIYORROLGFEEVSELQDPCYPIGRGFEALTALTDINGDLVDA 540
DB 481 GAPLFYEGORGRVFIYORROLGFEEVSELQDPCYPIGRGFEALTALTDINGDLVDA 540
QY 541 VGAPLEEQGAVYIFNGRHGGLSPQPSQRIEGTQVLSGIQWFGRSIHGVKDLBGDLADVA 600
DB 541 VGAPLEEQGAVYIFNGRHGGLSPQPSQRIEGTQVLSGIQWFGRSIHGVKDLBGDLADVA 600
QY 601 VGASQOMIVLSSRPVDMVTLMSPAPIPVHEVECSYSTSNKKEGVNITICQIKSLY 660
DB 601 VGASQOMIVLSSRPVDMVTLMSPAPIPVHEVECSYSTSNKKEGVNITICQIKSLY 660
QY 661 POGGRIVANLTYTLQDGHRTRRGLFPGGRHRLRNIATVTSMSCTDSFHPVCVOD 720
DB 661 POGGRIVANLTYTLQDGHRTRRGLFPGGRHRLRNIATVTSMSCTDSFHPVCVOD 720
QY 721 LISPINVSLNFSLWEEGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGEBKCEAN 780
DB 721 LISPINVSLNFSLWEEGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGEBKCEAN 780
QY 781 LRVSPSPARSRALRLTAPASISVELSNLEBDAYWOLDLHPPGGLSFRVEMLKPHSQ 840
DB 781 LRVSPSPARSRALRLTAPASISVELSNLEBDAYWOLDLHPPGGLSFRVEMLKPHSQ 840
QY 841 IIVSCBELPEBSRLSLRSLSCNVSSPIFKAGSHVALQMFENTLVNSSGDSVELHANVC 900
DB 841 IIVSCBELPEBSRLSLRSLSCNVSSPIFKAGSHVALQMFENTLVNSSGDSVELHANVC 900
QY 901 NNEBSDLLEDNASTTTIPIILYPINILIQDEBISTLYVSFTPKGPKIHQVKMIOVRIOPS 960
DB 901 NNEBSDLLEDNASTTTIPIILYPINILIQDEBISTLYVSFTPKGPKIHQVKMIOVRIOPS 960
QY 961 IHDNIPITLNAVGVPOPPSGPITTHQSVOMEPPVCHYEDLERLDAAPCLPGLALFR 1020
DB 961 IHDNIPITLNAVGVPOPPSGPITTHQSVOMEPPVCHYEDLERLDAAPCLPGLALFR 1020

```

```
Db 961 IHENIPTLEAVGVGPDPSESGPITHQWSVOMEPPVCHYEDLERLPPDAAPCLPGALFR 1020
Qy 1021 CPVVEROEILVQVIGTLELVEGEIEASSMFSLCSLSISFNSSKHFLYGSNASTLAQVVMK 1080
Db 1021 CPVVEROEILVQVIGTLELVEGEIEASSMFSLCSLSISFNSSKHFLYGSNASTLAQVVMK 1080
Qy 1081 VDVEYERKQMLYLYVLSIGIGLLLLIFIVLYKVGFPKRNLMKEKMEAGRGVNGIPADS 1140
Db 1081 VDVEYERKQMLYLYVLSIGIGLLLLIFIVLYKVGFPKRNLMKEKMEAGRGVNGIPADS 1140
Qy 1141 EQLASGQADPGCLKPLHKKDSBSGGKD 1170
Db 1141 EQLASGQADPGCLKPLHKKDSBSGGKD 1170
```

## RESULT 4

```
US-10-473-127-1743
; Sequence 1743, Application US/10473127
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1743
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-1743
```

```
Query Match 100.0%; Score 6106; DB 30; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MKDSCITVAMAMALLSGFFFPASSYNLDVGRARSFSPRAGRHRGVRVLOVNGVIVGA 60
Db 1 MKDSCITVAMAMALLSGFFFPASSYNLDVGRARSFSPRAGRHRGVRVLOVNGVIVGA 60
Qy 61 PGEKNSSTSLVQCOSGTHCLPVTLRGNSYTSKYLGMTLADPTDGSILACDPGLSRICD 120
Db 61 PGEKNSSTSLVQCOSGTHCLPVTLRGNSYTSKYLGMTLADPTDGSILACDPGLSRICD 120
Qy 121 QNTYLSGLCYFRQMLQGPMLQGRPGFOECIKANVDLFLPDGSMSLPDEROKTLDPMK 180
Db 121 QNTYLSGLCYFRQMLQGPMLQGRPGFOECIKANVDLFLPDGSMSLPDEROKTLDPMK 180
Qy 181 DVMKGLSNTSYQFAAVQSTSYKTEFSDVYKRDPAALKHVGMMLLNTTFGAINVY 240
Db 181 DVMKGLSNTSYQFAAVQSTSYKTEFSDVYKRDPAALKHVGMMLLNTTFGAINVY 240
Qy 241 ATEVPRELGRPADTKVLIIITDGEANDSGNIDAAKIIIRYIIGIGHFQTKESQETLH 300
Db 241 ATEVPRELGRPADTKVLIIITDGEANDSGNIDAAKIIIRYIIGIGHFQTKESQETLH 300
Qy 301 KFAASKPASEFVKILDTFEKLDLFTLQKJYIEGTSKODLTSFNMELSSGTSADLSR 360
Db 301 KFAASKPASEFVKILDTFEKLDLFTLQKJYIEGTSKODLTSFNMELSSGTSADLSR 360
Qy 361 GHAAVAVGAKDMAGGLDLKADLQDDTFIGNEPILPEVRAGVLYGVYTWLPSRQKTSLL 420
```

```
Db 361 GHAAVAVGAKDMAGGLDLKADLQDDTFIGNEPILPEVRAGVLYGVYTWLPSRQKTSLL 420
Qy 421 ASGAPRYOHMGRVLLPQEPQGGHWSOVOTIHQVQSYSGELCGVDVODGETELLII 480
Db 421 ASGAPRYOHMGRVLLPQEPQGGHWSOVOTIHQVQSYSGELCGVDVODGETELLII 480
Qy 481 GAPLFYGEORGRVFIQRRQLGFEESVSEQDPGYLGRFGAETALTIDINGDLVDA 540
Db 481 GAPLFYGEORGRVFIQRRQLGFEESVSEQDPGYLGRFGAETALTIDINGDLVDA 540
Qy 541 VGAPLEEQGAVYIFNGHGLSPQSORIGCTQVLSGIQWFGSIHGVKDLBGDLADVA 600
Db 541 VGAPLEEQGAVYIFNGHGLSPQSORIGCTQVLSGIQWFGSIHGVKDLBGDLADVA 600
Qy 601 VGAESQWIVLSSRPVVMQMLMSFPAEIVHVEGCSYSTSNMKEGVNTTICQIKSLY 660
Db 601 VGAESQWIVLSSRPVVMQMLMSFPAEIVHVEGCSYSTSNMKEGVNTTICQIKSLY 660
Qy 661 POFQGRIVANLTYTLQDGHRTTRRGLFPGARHRLRNIATVMSCTDFSFPFVVCVD 720
Db 661 POFQGRIVANLTYTLQDGHRTTRRGLFPGARHRLRNIATVMSCTDFSFPFVVCVD 720
Qy 721 LISPINVSLNFSLMBEETPRDQAGKDIPILRPSLHSEIWEIPEKXCGEDKCEAN 780
Db 721 LISPINVSLNFSLMBEETPRDQAGKDIPILRPSLHSEIWEIPEKXCGEDKCEAN 780
Qy 781 LRVSFSPARBARALRTFASLSVELSLNLEDAVWQDLHPPGISFPKVEMLKPHSQ 840
Db 781 LRVSFSPARBARALRTFASLSVELSLNLEDAVWQDLHPPGISFPKVEMLKPHSQ 840
Qy 841 IPVSCEELPEESRLSRLSCNVSPIFKAGHSVALQMFNTLVNSWGSVVELHANVTC 900
Db 841 IPVSCEELPEESRLSRLSCNVSPIFKAGHSVALQMFNTLVNSWGSVVELHANVTC 900
Qy 901 NNEDSDLLBNDSATTTIIPILYINILIQDEDSLYVSFTPKGPKIHQVHMTQVRIOPS 960
Db 901 NNEDSDLLBNDSATTTIIPILYINILIQDEDSLYVSFTPKGPKIHQVHMTQVRIOPS 960
Qy 961 IHENIPTLEAVGVGPDPSESGPITHQWSVOMEPPVCHYEDLERLPPDAAPCLPGALFR 1020
Db 961 IHENIPTLEAVGVGPDPSESGPITHQWSVOMEPPVCHYEDLERLPPDAAPCLPGALFR 1020
Qy 1021 CPVVEROEILVQVIGTLELVEGEIEASSMFSLCSLSISFNSSKHFLYGSNASTLAQVVMK 1080
Db 1021 CPVVEROEILVQVIGTLELVEGEIEASSMFSLCSLSISFNSSKHFLYGSNASTLAQVVMK 1080
Qy 1081 VDVEYERKQMLYLYVLSIGIGLLLLIFIVLYKVGFPKRNLMKEKMEAGRGVNGIPADS 1140
Db 1081 VDVEYERKQMLYLYVLSIGIGLLLLIFIVLYKVGFPKRNLMKEKMEAGRGVNGIPADS 1140
Qy 1141 EQLASGQADPGCLKPLHKKDSBSGGKD 1170
Db 1141 EQLASGQADPGCLKPLHKKDSBSGGKD 1170
```

## RESULT 5

```
PCT-US02-09671-1737
; Sequence 1737, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
```

```

PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1737
LENGTH: 1170
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09671-1737

Query Match      99.9%; Score 6098; DB 1; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVMAMALLSGFFFAFPASSYNDVGRASFSPPRAGRHHGYRLVQVNGVYGA 60
Db 1 MKDSCITVMAMALLSGFFFAFPASSYNDVGRASFSPPRAGRHHGYRLVQVNGVYGA 60

Qy 61 PGEKNSGSLVQCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Db 61 PGEKNSGSLVQCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120

Qy 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFQKILDFMK 180
Db 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFQKILDFMK 180

Qy 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFQKILDFMK 180
Db 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFQKILDFMK 180

Qy 181 DVNKKLSNTSYOFAAVOSTSYKTEPDSYVKMKDPALLKHVKNMLLNTTGAINYV 240
Db 181 DVNKKLSNTSYOFAAVOSTSYKTEPDSYVKMKDPALLKHVKNMLLNTTGAINYV 240

Qy 241 ATBVRREELGARPDATKYLIIITDGEATDGNIDAADIIIRYIIGIGHFQTKESQETLH 300
Db 241 ATBVRREELGARPDATKYLIIITDGEATDGNIDAADIIIRYIIGIGHFQTKESQETLH 300

Qy 301 KPASPRASEFYKILDFEKLKDLFELOKTYVEIGTSKODLTSTNMELSSGISADLSR 360
Db 301 KPASPRASEFYKILDFEKLKDLFELOKTYVEIGTSKODLTSTNMELSSGISADLSR 360

Qy 361 GHAVVAGVAGAKMDAGFLDLKADLDDDTFIGNEPILPEVRAGYLGATYTWLPSRKSTSL 420
Db 361 GHAVVAGVAGAKMDAGFLDLKADLDDDTFIGNEPILPEVRAGYLGATYTWLPSRKSTSL 420

Qy 421 ASQAPRYOHMGKRVLLFOBPQGGHMSQVQTHGTQIGSYFGGELCGVVDVDDGETELLII 480
Db 421 ASQAPRYOHMGKRVLLFOBPQGGHMSQVQTHGTQIGSYFGGELCGVVDVDDGETELLII 480

Qy 481 GAPLFYGRQGRGVITYORRQLGFEEVSELQDPPGYLGRFGEAITALTIDNGDLVVA 540
Db 481 GAPLFYGRQGRGVITYORRQLGFEEVSELQDPPGYLGRFGEAITALTIDNGDLVVA 540

Qy 541 VGAPLEEGGAVYIFNGRHGGLSPOPSORIEGTQVLSGIOMFGRSRHGVKDEGGLADVA 600
Db 541 VGAPLEEGGAVYIFNGRHGGLSPOPSORIEGTQVLSGIOMFGRSRHGVKDEGGLADVA 600

Qy 601 VGABEQMVLSSRPVDMVTILMSFSPAEIPIVHEVCSYSTSNKMEGNITITCFQIKSLY 660
Db 601 VGABEQMVLSSRPVDMVTILMSFSPAEIPIVHEVCSYSTSNKMEGNITITCFQIKSLY 660

Qy 661 POPQGRVLAANTLYTLQLDGHRTRRGGLPGGHEIRRNIAVTTSMSCDPSFHFVVCQD 720
Db 661 POPQGRVLAANTLYTLQLDGHRTRRGGLPGGHEIRRNIAVTTSMSCDPSFHFVVCQD 720

Qy 721 LIISPINVLNFSLWEEBGPDRQAKOIPILRPSLSHSTWELPFEKNCGEDKKCAN 780
Db 721 LIISPINVLNFSLWEEBGPDRQAKOIPILRPSLSHSTWELPFEKNCGEDKKCAN 780

Qy 781 LRVSPSPSRALRLTAFASSLVELSLNLEBEDAYVWLJLHPPGLSFRKVEMLKPSHQ 840
Db 781 LRVSPSPSRALRLTAFASSLVELSLNLEBEDAYVWLJLHPPGLSFRKVEMLKPSHQ 840

Qy 841 IIVSCBELPESRLSLRSLSCNVSSPIFKAGSHVALQMMFNTLVNNSMGDSVELHANTYC 900
Db 841 IIVSCBELPESRLSLRSLSCNVSSPIFKAGSHVALQMMFNTLVNNSMGDSVELHANTYC 900

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841 IIVSCBELPESRLSLRSLSCNVSSPIFKAGSHVALQMMFNTLVNNSMGDSVELHANTYC 900
901 NNEBDDLEDNSATTIIPILYINILLIQDEESTLYVSPFKGKIHQVKMYQVRIOPS 960
901 NNEBDDLEDNSATTIIPILYINILLIQDEESTLYVSPFKGKIHQVKMYQVRIOPS 960
961 IHDNIPITLNAVVPQPPSPBGPITTHQMSVQMEPPVCHIEDLERLDAAEPCLPGLFR 1020
961 IHDNIPITLNAVVPQPPSPBGPITTHQMSVQMEPPVCHIEDLERLDAAEPCLPGLFR 1020
1021 CPVVFROBILYQVGTLELVEIRASSMFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080
1021 CPVVFROBILYQVGTLELVEIRASSMFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080
1081 VDVIYKQMLYLYLSGIGILLILLIFVLVYKVFERNLKEKMEAGRVNGIPAEBS 1140
1081 VDVIYKQMLYLYLSGIGILLILLIFVLVYKVFERNLKEKMEAGRVNGIPAEBS 1140
1141 EQLASQOBADPGCLKFLHEDSBSGGKD 1170
1141 EQLASQOBADPGCLKFLHEDSBSGGKD 1170

RESULT 6
PCT-US02-09671-1739
Sequence 1739, Application PC/TUS0209671
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: PCT/US02/09671
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1739
LENGTH: 1170
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09671-1739

Query Match      99.9%; Score 6098; DB 1; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVMAMALLSGFFFAFPASSYNDVGRASFSPPRAGRHHGYRLVQVNGVYGA 60
Db 1 MKDSCITVMAMALLSGFFFAFPASSYNDVGRASFSPPRAGRHHGYRLVQVNGVYGA 60

Qy 61 PGEKNSGSLVQCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120
Db 61 PGEKNSGSLVQCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120

Qy 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFQKILDFMK 180
Db 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFQKILDFMK 180

Qy 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFQKILDFMK 180
Db 121 QNTYLSGICYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFQKILDFMK 180

Qy 181 DVNKKLSNTSYOFAAVOSTSYKTEPDSYVKMKDPALLKHVKNMLLNTTGAINYV 240
Db 181 DVNKKLSNTSYOFAAVOSTSYKTEPDSYVKMKDPALLKHVKNMLLNTTGAINYV 240

```

QY 241 ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADKIIIRYIIGIGKHFQTKESQETLH 300  
DB 241 ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADKIIIRYIIGIGKHFQTKESQETLH 300  
QY 301 KFAKSPASEFVKIILDTFEKLDLFTLEOKKIYVIEGSKODLTSFNNELSSSGISADLSR 360  
DB 301 KFAKSPASEFVKIILDTFEKLDLFTLEOKKIYVIEGSKODLTSFNNELSSSGISADLSR 360  
QY 361 GHAVVAGAKDMAGGFLDLKADLQDDTFIGNBPLPEVRAGYLYGYVTWMLPSROKTSLL 420  
DB 361 GHAVVAGAKDMAGGFLDLKADLQDDTFIGNBPLPEVRAGYLYGYVTWMLPSROKTSLL 420  
QY 421 ASGARPYOHMGRVLLFOEPGGGHSQVOTIHGTQIGSYFGGELCGVDVDDQGETELLII 480  
DB 421 ASGARPYOHMGRVLLFOEPGGGHSQVOTIHGTQIGSYFGGELCGVDVDDQGETELLII 480  
QY 481 GAPLFYEGORGRVFIYORROLGFEVSELOQDPGYLGRGEGALITLTDINGGLADVA 540  
DB 481 GAPLFYEGORGRVFIYORROLGFEVSELOQDPGYLGRGEGALITLTDINGGLADVA 540  
QY 541 VGAPLEEGAVYIFNGRHGGLSPOPSORIEGTOVLSGIQWFGRSIHGVKDLBGGLADVA 600  
DB 541 VGAPLEEGAVYIFNGRHGGLSPOPSORIEGTOVLSGIQWFGRSIHGVKDLBGGLADVA 600  
QY 601 VGASQMIIVLSRPVDMVTLMSPSPALIPVHEVSCYSTSNKMEGVNITICFOIKSLY 660  
DB 601 VGASQMIIVLSRPVDMVTLMSPSPALIPVHEVSCYSTSNKMEGVNITICFOIKSLY 660  
QY 661 POFQGRIVANULTYTLQDGHRTRRGLFPGGRHLEARNIAVTTSMSCTDPSFHPVCQD 720  
DB 661 POFQGRIVANULTYTLQDGHRTRRGLFPGGRHLEARNIAVTTSMSCTDPSFHPVCQD 720  
QY 721 LISPINVLSNLSMEEBGTPRDQAOQKDIPIILPSLHSETWELPFKNGCEDKCCAN 780  
DB 721 LISPINVLSNLSMEEBGTPRDQAOQKDIPIILPSLHSETWELPFKNGCEDKCCAN 780  
QY 781 LRVSPSPARSALRLTAFASLSVELSLNLEBDAYWQDLHFPFGLSFRKVENMLKPHSQ 840  
DB 781 LRVSPSPARSALRLTAFASLSVELSLNLEBDAYWQDLHFPFGLSFRKVENMLKPHSQ 840  
QY 841 IPVSCBEPBSRLISRLSCNVSSPIFKAGHSVALQMMFNTLVNNSGSDSVEHLANTYC 900  
DB 841 IPVSCBEPBSRLISRLSCNVSSPIFKAGHSVALQMMFNTLVNNSGSDSVEHLANTYC 900  
QY 901 NNEBSDLLEDNSATITIPILYPINILIDODSDSTLYSFTPKGPIIHOVKMYOVRLOPS 960  
DB 901 NNEBSDLLEDNSATITIPILYPINILIDODSDSTLYSFTPKGPIIHOVKMYOVRLOPS 960  
QY 961 IHDNRIPTLEAVGVPOPSBGPITTHQMSVQMEBPVPCHEYDLERLPDAEPCLPGALFR 1020  
DB 961 IHDNRIPTLEAVGVPOPSBGPITTHQMSVQMEBPVPCHEYDLERLPDAEPCLPGALFR 1020  
QY 1021 CPVYFRQGIILVOYGTLELVGEIEASMSFSLCSSISIFNSSKIHHLXGNSASLAQVYMK 1080  
DB 1021 CPVYFRQGIILVOYGTLELVGEIEASMSFSLCSSISIFNSSKIHHLXGNSASLAQVYMK 1080  
QY 1081 DVVYVEKQMLTYLYLSGIGLLLLLIPIYLYKVGFPKRNLEKKEAGRGVNGIPADS 1140  
DB 1081 DVVYVEKQMLTYLYLSGIGLLLLLIPIYLYKVGFPKRNLEKKEAGRGVNGIPADS 1140  
QY 1141 EQLASGQAGDPGCLKPLHEKDSGSGKGD 1170  
DB 1141 EQLASGQAGDPGCLKPLHEKDSGSGKGD 1170

RESULT 7  
PCT-US02-09671-1742  
; Sequence 1742, Application PC/TUS0209671  
; GENERAL INFORMATION:

; APPLICANT: Zycoos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: PCT/US02/09671

;; CURRENT FILING DATE: 2002-03-28  
;; PRIOR APPLICATION NUMBER: 60/279,495  
;; PRIOR FILING DATE: 2001-03-28  
;; PRIOR APPLICATION NUMBER: 60/292,544  
;; PRIOR FILING DATE: 2001-05-21  
;; PRIOR APPLICATION NUMBER: 60/310,801  
;; PRIOR FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: 60/326,370  
;; PRIOR FILING DATE: 2001-10-01  
;; PRIOR APPLICATION NUMBER: 60/336,780  
;; PRIOR FILING DATE: 2001-12-04  
;; PRIOR APPLICATION NUMBER: 60/358,985  
;; PRIOR FILING DATE: 2002-02-20  
;; NUMBER OF SEQ ID NOS: 2041  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1742  
;; LENGTH: 1170  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
PCT-US02-09671-1742

Query Match 99.9%; Score 6098; DB 1; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKOSCIIVMMAMALISGFFFPAPASSYNLVDRGARSFSPRAGHFGYRVLOVNGVIVGA 60  
DB 1 MKOSCIIVMMAMALISGFFFPAPASSYNLVDRGARSFSPRAGHFGYRVLOVNGVIVGA 60  
QY 61 PGBGNSYSGSLYQCSGSGHCLPVTLRGNSYTSKYLGMTLATDPTDGSIIACDPLSRTCD 120  
DB 61 PGBGNSYSGSLYQCSGSGHCLPVTLRGNSYTSKYLGMTLATDPTDGSIIACDPLSRTCD 120  
QY 121 QNTYLSGLCYLFRQNLQCPMLQGRPGROBCKGNVULVFLPDSMSIQDPDEFQKILDFMK 180  
DB 121 QNTYLSGLCYLFRQNLQCPMLQGRPGROBCKGNVULVFLPDSMSIQDPDEFQKILDFMK 180  
QY 181 DVMKLSNTSYQFAAVOFSTSYKTEFPFSDYVRKDPDALLKHYKMLLTNTFGAINVY 240  
DB 181 DVMKLSNTSYQFAAVOFSTSYKTEFPFSDYVRKDPDALLKHYKMLLTNTFGAINVY 240  
QY 241 ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADKIIIRYIIGIGKHFQTKESQETLH 300  
DB 241 ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADKIIIRYIIGIGKHFQTKESQETLH 300  
QY 301 KFAKSPASEFVKIILDTFEKLDLFTLEOKKIYVIEGSKODLTSFNNELSSSGISADLSR 360  
DB 301 KFAKSPASEFVKIILDTFEKLDLFTLEOKKIYVIEGSKODLTSFNNELSSSGISADLSR 360  
QY 361 GHAVVAGAKDMAGGFLDLKADLQDDTFIGNBPLPEVRAGYLYGYVTWMLPSROKTSLL 420  
DB 361 GHAVVAGAKDMAGGFLDLKADLQDDTFIGNBPLPEVRAGYLYGYVTWMLPSROKTSLL 420  
QY 421 ASGARPYOHMGRVLLFOEPGGGHSQVOTIHGTQIGSYFGGELCGVDVDDQGETELLII 480  
DB 421 ASGARPYOHMGRVLLFOEPGGGHSQVOTIHGTQIGSYFGGELCGVDVDDQGETELLII 480  
QY 481 GAPLFYEGORGRVFIYORROLGFEVSELOQDPGYLGRGEGALITLTDINGGLADVA 540  
DB 481 GAPLFYEGORGRVFIYORROLGFEVSELOQDPGYLGRGEGALITLTDINGGLADVA 540  
QY 541 VGAPLEEGAVYIFNGRHGGLSPOPSORIEGTOVLSGIQWFGRSIHGVKDLBGGLADVA 600  
DB 541 VGAPLEEGAVYIFNGRHGGLSPOPSORIEGTOVLSGIQWFGRSIHGVKDLBGGLADVA 600  
QY 601 VGASQMIIVLSRPVDMVTLMSPSPALIPVHEVSCYSTSNKMEGVNITICFOIKSLY 660  
DB 601 VGASQMIIVLSRPVDMVTLMSPSPALIPVHEVSCYSTSNKMEGVNITICFOIKSLY 660  
QY 661 POFQGRIVANULTYTLQDGHRTRRGLFPGGRHLEARNIAVTTSMSCTDPSFHPVCQD 720  
DB 661 POFQGRIVANULTYTLQDGHRTRRGLFPGGRHLEARNIAVTTSMSCTDPSFHPVCQD 720

QY 721 LISPINVSLNFWBEGTFRDQAOQKDIPIILRPSLHSETWEIPEKNGCEBKCCAN 780  
DB 721 LISPINVSLNFWBEGTFRDQAOQKDIPIILRPSLHSETWEIPEKNGCEBKCCAN 780  
QY 781 LRVSPARSRALRLTAFASISVELSLNLEBDAYWQDLHFPFGLSFRKVEMLKPHSQ 840  
DB 781 LRVSPARSRALRLTAFASISVELSLNLEBDAYWQDLHFPFGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCEELPEBSRLSRALSCNVSPIFKAGHSVALQMMFNTLVNWSWGDSVELHANTVC 900  
DB 841 IPVSCEELPEBSRLSRALSCNVSPIFKAGHSVALQMMFNTLVNWSWGDSVELHANTVC 900  
QY 901 NNEDSDLEEDNSATTTIPIILPINILIQDQEDSTLYVSPFKGPKIHQVKMYOVRLOPS 960  
DB 901 NNEDSDLEEDNSATTTIPIILPINILIQDQEDSTLYVSPFKGPKIHQVKMYOVRLOPS 960  
QY 961 IHDNIPITLEAVGVPOPPSEGPITHQMSVOMEPPVCHYEDLERLPDAEPCLPGALFR 1020  
DB 961 IHDNIPITLEAVGVPOPPSEGPITHQMSVOMEPPVCHYEDLERLPDAEPCLPGALFR 1020  
QY 1021 CPVVRQELIIVQIGTLELVGEIEASMFSLCSSLSISFNSSKPHFLYGSNASLAQVVMK 1080  
DB 1021 CPVVRQELIIVQIGTLELVGEIEASMFSLCSSLSISFNSSKPHFLYGSNASLAQVVMK 1080  
QY 1081 VDVIYERKQMLYLYLSIGIGILLLLITVLYKYGFRRNLKEKMEAGRGVPNGI PAEDS 1140  
DB 1081 VDVIYERKQMLYLYLSIGIGILLLLITVLYKYGFRRNLKEKMEAGRGVPNGI PAEDS 1140  
QY 1141 EQLASGOEAGDPGCLKPLHEKDSBESGGKD 1170  
DB 1141 EQLASGOEAGDPGCLKPLHEKDSBESGGKD 1170

## RESULT 8

PCT-US03-12946-3007  
Sequence 3007, Application PC/TUS0312946  
GENERAL INFORMATION:  
APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
APPLICANT: Wohlgemuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
APPLICANT: Prentice, James  
APPLICANT: Morris, Macdonald  
APPLICANT: Rosenberg, Steven  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
FILE REFERENCE: 506612000150  
CURRENT APPLICATION NUMBER: PCT/US03/12946  
CURRENT FILING DATE: 2003-04-24  
PRIOR APPLICATION NUMBER: US 10/131,827  
PRIOR FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 10/325,899  
NUMBER OF SEQ ID NOS: 3117  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3007  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US03-12946-3007

Query Match 99.9%; Score 6098; DB 1; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITTMAMALLSGFFFPAPASSYNDVRCARFSPPRAGRHFGRVYLOYGVNVIYGA 60  
DB 1 MKDSCITTMAMALLSGFFFPAPASSYNDVRCARFSPPRAGRHFGRVYLOYGVNVIYGA 60  
QY 61 PEGGNSSTSLVOCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120  
DB 61 PEGGNSSTSLVOCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120

QY 121 QNTYLSGLCYLFRONTLOQPMLOGRPROECKIGNVDLVFLPDSMSLOPDEFOKILDEMK 180  
DB 121 QNTYLSGLCYLFRONTLOQPMLOGRPROECKIGNVDLVFLPDSMSLOPDEFOKILDEMK 180  
QY 181 DVMKGLSNTSYQFAAVOFTSYKTEFPDSDYVRKDDALLKHKHMLLTNTFGAINVY 240  
DB 181 DVMKGLSNTSYQFAAVOFTSYKTEFPDSDYVRKDDALLKHKHMLLTNTFGAINVY 240  
QY 241 ATEVFRBELGARDPATVLLIITDGEATDSGNIDAADRIIYIIGIKHFOTKESQETLH 300  
DB 241 ATEVFRBELGARDPATVLLIITDGEATDSGNIDAADRIIYIIGIKHFOTKESQETLH 300  
QY 301 KPAKSPASEFYKILIDTEKIKDLFTELQKTIYVEGTSKODLPSFNNELSSSGISADLSR 360  
DB 301 KPAKSPASEFYKILIDTEKIKDLFTELQKTIYVEGTSKODLPSFNNELSSSGISADLSR 360  
QY 361 GHAVVAVGAKDMAGFLDKADLODDPTIIGNEPLTEVAVAGYUGYVTWMLPSRQKTSLL 420  
DB 361 GHAVVAVGAKDMAGFLDKADLODDPTIIGNEPLTEVAVAGYUGYVTWMLPSRQKTSLL 420  
QY 421 ASGAPRYOHNGRVLLFOEPQGGHMSQVOTIHGTQISYFEGELCGVDVDDGETELLII 480  
DB 421 ASGAPRYOHNGRVLLFOEPQGGHMSQVOTIHGTQISYFEGELCGVDVDDGETELLII 480  
QY 481 GAPLFYGEORGRVFIYORQOLGFEVYSELQDPGTYLGRGEMALTLDINGGLYDVA 540  
DB 481 GAPLFYGEORGRVFIYORQOLGFEVYSELQDPGTYLGRGEMALTLDINGGLYDVA 540  
QY 541 VGAPLEBOGAVYIFNGRHGGLSPQSORIGTOVLSGIOMFGRSIHGVKDLBEGGLADVA 600  
DB 541 VGAPLEBOGAVYIFNGRHGGLSPQSORIGTOVLSGIOMFGRSIHGVKDLBEGGLADVA 600  
QY 601 VGASQMIIVLSRPPVDMVTLMSFSPALIPVHEVECSYSTSNKKEGVNITTCQIKSLY 660  
DB 601 VGASQMIIVLSRPPVDMVTLMSFSPALIPVHEVECSYSTSNKKEGVNITTCQIKSLY 660  
QY 661 POFQGRIVANITYTLQDGHRTTRRGLPGGRHRLRNIAVTTSMSCCTDPSFHPVCVD 720  
DB 661 POFQGRIVANITYTLQDGHRTTRRGLPGGRHRLRNIAVTTSMSCCTDPSFHPVCVD 720  
QY 721 LISPINVSLNFWBEGTFRDQAOQKDIPIILRPSLHSETWEIPEKNGCEBKCCAN 780  
DB 721 LISPINVSLNFWBEGTFRDQAOQKDIPIILRPSLHSETWEIPEKNGCEBKCCAN 780  
QY 781 LRVSPARSRALRLTAFASISVELSLNLEBDAYWQDLHFPFGLSFRKVEMLKPHSQ 840  
DB 781 LRVSPARSRALRLTAFASISVELSLNLEBDAYWQDLHFPFGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCEELPEBSRLSRALSCNVSPIFKAGHSVALQMMFNTLVNWSWGDSVELHANTVC 900  
DB 841 IPVSCEELPEBSRLSRALSCNVSPIFKAGHSVALQMMFNTLVNWSWGDSVELHANTVC 900  
QY 901 NNEDSDLEEDNSATTTIPIILPINILIQDQEDSTLYVSPFKGPKIHQVKMYOVRLOPS 960  
DB 901 NNEDSDLEEDNSATTTIPIILPINILIQDQEDSTLYVSPFKGPKIHQVKMYOVRLOPS 960  
QY 961 IHDNIPITLEAVGVPOPPSEGPITHQMSVOMEPPVCHYEDLERLPDAEPCLPGALFR 1020  
DB 961 IHDNIPITLEAVGVPOPPSEGPITHQMSVOMEPPVCHYEDLERLPDAEPCLPGALFR 1020  
QY 1021 CPVVRQELIIVQIGTLELVGEIEASMFSLCSSLSISFNSSKPHFLYGSNASLAQVVMK 1080  
DB 1021 CPVVRQELIIVQIGTLELVGEIEASMFSLCSSLSISFNSSKPHFLYGSNASLAQVVMK 1080  
QY 1081 VDVIYERKQMLYLYLSIGIGILLLLITVLYKYGFRRNLKEKMEAGRGVPNGI PAEDS 1140  
DB 1081 VDVIYERKQMLYLYLSIGIGILLLLITVLYKYGFRRNLKEKMEAGRGVPNGI PAEDS 1140  
QY 1141 EQLASGOEAGDPGCLKPLHEKDSBESGGKD 1170  
DB 1141 EQLASGOEAGDPGCLKPLHEKDSBESGGKD 1170

RESULT 9  
PCT-US03-40978-1088  
; Sequence 1088, Application EC/TUS0340978  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CLO01499 MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; CURRENT FILING DATE: 2003-12-22  
; CURRENT FILING DATE: 2003-12-22  
; SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0  
; SEQ ID NO 1088  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-40978-1088

Query Match 99.9%; Score 6098; DB 1; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVRGASFSPPRAGRHFGRVLOVANGVIGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVRGASFSPPRAGRHFGRVLOVANGVIGA 60
OY 61 PGBGNSGSLYOCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSTCD 120
DB 61 PGBGNSGSLYOCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSTCD 120
OY 121 QNTYLSGLCYLFRNLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFOKILDPMK 180
DB 121 QNTYLSGLCYLFRNLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFOKILDPMK 180
OY 181 DVMKLSTSYQPAAVQSTSYKTEFDFSDYKRDPAALDKHVKMLLNTFGAINV 240
DB 181 DVMKLSTSYQPAAVQSTSYKTEFDFSDYKRDPAALDKHVKMLLNTFGAINV 240
OY 241 ATEVREBELGARPRATKYLIIITGEATDSGNIDAKOIIIRIIGIGKFPQKSOETLH 300
DB 241 ATEVREBELGARPRATKYLIIITGEATDSGNIDAKOIIIRIIGIGKFPQKSOETLH 300
OY 301 KFAKSPASEFYKILDTFEKLDLFTLOKLIYVIGTSKODLTSFNMELSSSGISADLSR 360
DB 301 KFAKSPASEFYKILDTFEKLDLFTLOKLIYVIGTSKODLTSFNMELSSSGISADLSR 360
OY 361 GHAVVGAAGVADWAGGFLDLKADLODDTFIGNEPITPEVRAGYIGYIVTWLPSROKISLL 420
DB 361 GHAVVGAAGVADWAGGFLDLKADLODDTFIGNEPITPEVRAGYIGYIVTWLPSROKISLL 420
OY 421 ASGARVYOHMRVLLFQEPQGGHMSQVQTHIGQISYFGGELCGVVDODGETELLII 480
DB 421 ASGARVYOHMRVLLFQEPQGGHMSQVQTHIGQISYFGGELCGVVDODGETELLII 480
OY 481 GAPLFYGBORGRVFIYORROLGFEFVSELQDPEYPIGRFGEATLTALTDINGDLVVA 540
DB 481 GAPLFYGBORGRVFIYORROLGFEFVSELQDPEYPIGRFGEATLTALTDINGDLVVA 540
OY 541 VGABIEBOGAVYIFNGRHGSLSPQSPQRIEGTVLSGIQWFGRSIHGVKLEBGLADVA 600
DB 541 VGABIEBOGAVYIFNGRHGSLSPQSPQRIEGTVLSGIQWFGRSIHGVKLEBGLADVA 600
OY 601 VGABSQMTVLSSRPVMDVMTLMSFPAIPVHEVBCSYSTSNKMEGVNITICFOIKSLI 660
DB 601 VGABSQMTVLSSRPVMDVMTLMSFPAIPVHEVBCSYSTSNKMEGVNITICFOIKSLI 660
OY 661 POFQGRVAVANTYTLQDLGHRTRRGLPPGGRHELRNIAVTTSMSCDTSFHFVVCOD 720
DB 661 POFQGRVAVANTYTLQDLGHRTRRGLPPGGRHELRNIAVTTSMSCDTSFHFVVCOD 720
OY 721 LISPIVNSLNFSLWEEGTPRDOAOKDIPPIILPSLHSETWEIPPEKNCGBDKCEAN 780
DB 721 LISPIVNSLNFSLWEEGTPRDOAOKDIPPIILPSLHSETWEIPPEKNCGBDKCEAN 780
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DB 721 LISPIVNSLNFSLWEEGTPRDOAOKDIPPIILPSLHSETWEIPPEKNCGBDKCEAN 780
OY 781 LRVSPARARALRTAPASTSYELSLNLEBAYWVQULHPPPGSPKRVEMLKPSHQ 840
DB 781 LRVSPARARALRTAPASTSYELSLNLEBAYWVQULHPPPGSPKRVEMLKPSHQ 840
OY 841 IVPSCBELPRESRLSALSCNVSPIFKAGHSVALQMMNTLVNSWGDVBLHANVTC 900
DB 841 IVPSCBELPRESRLSALSCNVSPIFKAGHSVALQMMNTLVNSWGDVBLHANVTC 900
OY 901 NNEDSDLEENSATTIIPILYPINILIQODEDSTLYSFPKPKKHQVHMVQVRQPS 960
DB 901 NNEDSDLEENSATTIIPILYPINILIQODEDSTLYSFPKPKKHQVHMVQVRQPS 960
OY 961 IHDNIPITLNAVGVPOPPSEGPITTHQWSQVMEPPVCHIEDLRLPDAEPCPGALFR 1020
DB 961 IHDNIPITLNAVGVPOPPSEGPITTHQWSQVMEPPVCHIEDLRLPDAEPCPGALFR 1020
OY 1021 CPVVFROEILVQVIGTLELVGEIEASSMFSLSISFNSKHFLYGSNASIAQVVMK 1080
DB 1021 CPVVFROEILVQVIGTLELVGEIEASSMFSLSISFNSKHFLYGSNASIAQVVMK 1080
OY 1081 VDVIYERQMTLYLTLGIGLLILLIFLYLYKVGFKRMUKKMEAGRGVPNGIPAEBS 1140
DB 1081 VDVIYERQMTLYLTLGIGLLILLIFLYLYKVGFKRMUKKMEAGRGVPNGIPAEBS 1140
OY 1141 EQLASGOEAGDPGLCKPLHKDSSESGGKD 1170
DB 1141 EQLASGOEAGDPGLCKPLHKDSSESGGKD 1170
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RESULT 10  
US-09-592-617A-42  
; Sequence 42, Application US/09592617A  
; GENERAL INFORMATION:  
; APPLICANT: Airtaout, M. Armin  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS  
; FILE REFERENCE: 00786-267002  
; CURRENT FILING DATE: US/09/592,617A  
; PRIOR FILING DATE: 2000-06-13  
; PRIOR APPLICATION NUMBER: US 08/380,167  
; PRIOR FILING DATE: 1999-01-30  
; PRIOR APPLICATION NUMBER: US 08/216,081  
; PRIOR FILING DATE: 1994-03-21  
; PRIOR APPLICATION NUMBER: US 07/637,830  
; PRIOR FILING DATE: 1991-01-04  
; PRIOR APPLICATION NUMBER: US 07/539,842  
; PRIOR FILING DATE: 1990-06-18  
; PRIOR APPLICATION NUMBER: US 07/212,573  
; PRIOR FILING DATE: 1988-06-28  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0  
; SEQ ID NO 42  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-592-617A-42

Query Match 99.9%; Score 6098; DB 19; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVRGASFSPPRAGRHFGRVLOVANGVIGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVRGASFSPPRAGRHFGRVLOVANGVIGA 60
OY 61 PGBGNSGSLYOCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSTCD 120
DB 61 PGBGNSGSLYOCOSGTHCLPVTLRGSNTSKYLGMTLATDPTDGSILACDPGLSTCD 120
OY 121 QNTYLSGLCYLFRNLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFOKILDPMK 180
DB 121 QNTYLSGLCYLFRNLQGPMLQGRPGFQECIKGNVDLVFLFDGSMSLQDPDFOKILDPMK 180
OY 181 DVVKERQMTLYLTLGIGLLILLIFLYLYKVGFKRMUKKMEAGRGVPNGIPAEBS 1140
DB 181 DVVKERQMTLYLTLGIGLLILLIFLYLYKVGFKRMUKKMEAGRGVPNGIPAEBS 1140
OY 1141 EQLASGOEAGDPGLCKPLHKDSSESGGKD 1170
DB 1141 EQLASGOEAGDPGLCKPLHKDSSESGGKD 1170
```

QY 181 DVMKLSNTSYQFAAVOFSTSYKTEPFSDVYKRDPAALLKHVKNMLLTTTGAINVY 240  
DB 181 DVMKLSNTSYQFAAVOFSTSYKTEPFSDVYKRDPAALLKHVKNMLLTTTGAINVY 240  
QY 241 ATEVERREELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIGIKHFQTKESQETLH 300  
DB 241 ATEVERREELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIGIKHFQTKESQETLH 300  
QY 301 KFAASKPASEFVKIILDTFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSGISAADLSR 360  
DB 301 KFAASKPASEFVKIILDTFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSGISAADLSR 360  
QY 361 GHAVVAVGAKDMAGGFLDKADLDDDFIIGNEPLTPEVRAGYLGYYTWMJPSRQKTSIL 420  
DB 361 GHAVVAVGAKDMAGGFLDKADLDDDFIIGNEPLTPEVRAGYLGYYTWMJPSRQKTSIL 420  
QY 421 ASGARPYOHMGRVLLFQEPQGGGHSOVQTIHGTOIGSYFGGELGVDVDDOGTELLLI 480  
DB 421 ASGARPYOHMGRVLLFQEPQGGGHSOVQTIHGTOIGSYFGGELGVDVDDOGTELLLI 480  
QY 481 GAPLFYGBORGRVFIYORRQLGFEVEVELQDPCGYLGRFGEAITALTDINGDLVDA 540  
DB 481 GAPLFYGBORGRVFIYORRQLGFEVEVELQDPCGYLGRFGEAITALTDINGDLVDA 540  
QY 541 VGAPLEBEGGAVYIENGHRGGLSPQSPORIEGTQVLSGIQWFGRSIHGYKDLBEGDLADVA 600  
DB 541 VGAPLEBEGGAVYIENGHRGGLSPQSPORIEGTQVLSGIQWFGRSIHGYKDLBEGDLADVA 600  
QY 601 VGASQMIIVLSSRPVDMVTLMSPSPARIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
DB 601 VGASQMIIVLSSRPVDMVTLMSPSPARIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
QY 661 POFQGRVLANLTYTLQLDGHRTRRRGLFPGGRHELRNIAVTTSMSCDTSFHFVVCQD 720  
DB 661 POFQGRVLANLTYTLQLDGHRTRRRGLFPGGRHELRNIAVTTSMSCDTSFHFVVCQD 720  
QY 721 LIISPIVNSLNTSLMEEBEGTPRQDQAKODIPILPISLHSETWBIPEFKNCGEKKCEAN 780  
DB 721 LIISPIVNSLNTSLMEEBEGTPRQDQAKODIPILPISLHSETWBIPEFKNCGEKKCEAN 780  
QY 781 LRVSPSPRSRLRLTAFAASLVELSLNLEBDAYWOLDLHPPRGLSPRKVEMLKPHSQ 840  
DB 781 LRVSPSPRSRLRLTAFAASLVELSLNLEBDAYWOLDLHPPRGLSPRKVEMLKPHSQ 840  
QY 841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAHSHVALQMMFNTLVNWSGDSVELHANVTC 900  
DB 841 IPVSCBELPEBSRLLSRALSCNVSSPIFKAHSHVALQMMFNTLVNWSGDSVELHANVTC 900  
QY 901 NNBDSDLEBNSATTIIPILYPINILIODQEDSTLYSFTPKGPKIHQVKAMYQVRIOPS 960  
DB 901 NNBDSDLEBNSATTIIPILYPINILIODQEDSTLYSFTPKGPKIHQVKAMYQVRIOPS 960  
QY 961 IHDNHIPTLEAVNGVPOPPSEBPTIHOVSVQMEPPVPCHYEDLELPPAABECLPGLAFR 1020  
DB 961 IHDNHIPTLEAVNGVPOPPSEBPTIHOVSVQMEPPVPCHYEDLELPPAABECLPGLAFR 1020  
QY 1021 CPVYVROEILVOVIGTLEVEIEASSMFSLCSSISIFNSKIHPLVGSNBSLAQVVMK 1080  
DB 1021 CPVYVROEILVOVIGTLEVEIEASSMFSLCSSISIFNSKIHPLVGSNBSLAQVVMK 1080  
QY 1081 VDVIYVEKQMLYLYVLSGIGLLLIIFIVLYKVGFPRKNLKEKWEAGRGVNGIPADS 1140  
DB 1081 VDVIYVEKQMLYLYVLSGIGLLLIIFIVLYKVGFPRKNLKEKWEAGRGVNGIPADS 1140  
QY 1141 BOLASGOBAGDPCCLKPLHEKDSBSGGKD 1170  
DB 1141 BOLASGOBAGDPCCLKPLHEKDSBSGGKD 1170

RESULT 11  
US-09-592-617C-42  
; Sequence 42, Application US/09592617C

GENERAL INFORMATION:  
; APPLICANT: Armout, M. Armit  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS  
; FILE REFERENCE: 00786-267002  
; CURRENT APPLICATION NUMBER: US/09/592,617C  
; PRIOR FILING DATE: 2000-06-13  
; PRIOR APPLICATION NUMBER: US 08/380,167  
; PRIOR FILING DATE: 1999-01-30  
; PRIOR APPLICATION NUMBER: US 08/216,081  
; PRIOR FILING DATE: 1994-03-21  
; PRIOR APPLICATION NUMBER: US 07/637,830  
; PRIOR FILING DATE: 1991-01-04  
; PRIOR APPLICATION NUMBER: US 07/539,842  
; PRIOR FILING DATE: 1990-06-18  
; PRIOR APPLICATION NUMBER: US 07/212,573  
; PRIOR FILING DATE: 1988-06-28  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-592-617C-42

Query Match 99.9%; Score 6098; DB 19; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITYMAMALLSGFFFPAPASYNLDVGAHSFSPRAGRHFGRVLOVNGVYGA 60  
DB 1 MKDSCITYMAMALLSGFFFPAPASYNLDVGAHSFSPRAGRHFGRVLOVNGVYGA 60  
QY 61 PEGNSGSLYQCSGTHCLPVTLRGNTSKYLGMTLATDPTDGSILACDPLSRD 120  
DB 61 PEGNSGSLYQCSGTHCLPVTLRGNTSKYLGMTLATDPTDGSILACDPLSRD 120  
QY 121 QNTYLSGLCYLFRONLQPMLOGRPGQECIKGNVDLVFLPDGSMISQPDFQKILDFMK 180  
DB 121 QNTYLSGLCYLFRONLQPMLOGRPGQECIKGNVDLVFLPDGSMISQPDFQKILDFMK 180  
QY 181 DVMKLSNTSYQFAAVOFSTSYKTEPFSDVYKRDPAALLKHVKNMLLTTTGAINVY 240  
DB 181 DVMKLSNTSYQFAAVOFSTSYKTEPFSDVYKRDPAALLKHVKNMLLTTTGAINVY 240  
QY 241 ATEVERREELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIGIKHFQTKESQETLH 300  
DB 241 ATEVERREELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIGIKHFQTKESQETLH 300  
QY 301 KFAASKPASEFVKIILDTFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSGISAADLSR 360  
DB 301 KFAASKPASEFVKIILDTFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSGISAADLSR 360  
QY 361 GHAVVAVGAKDMAGGFLDKADLDDDFIIGNEPLTPEVRAGYLGYYTWMJPSRQKTSIL 420  
DB 361 GHAVVAVGAKDMAGGFLDKADLDDDFIIGNEPLTPEVRAGYLGYYTWMJPSRQKTSIL 420  
QY 421 ASGARPYOHMGRVLLFQEPQGGGHSOVQTIHGTOIGSYFGGELGVDVDDOGTELLLI 480  
DB 421 ASGARPYOHMGRVLLFQEPQGGGHSOVQTIHGTOIGSYFGGELGVDVDDOGTELLLI 480  
QY 481 GAPLFYGBORGRVFIYORRQLGFEVEVELQDPCGYLGRFGEAITALTDINGDLVDA 540  
DB 481 GAPLFYGBORGRVFIYORRQLGFEVEVELQDPCGYLGRFGEAITALTDINGDLVDA 540  
QY 541 VGAPLEBEGGAVYIENGHRGGLSPQSPORIEGTQVLSGIQWFGRSIHGYKDLBEGDLADVA 600  
DB 541 VGAPLEBEGGAVYIENGHRGGLSPQSPORIEGTQVLSGIQWFGRSIHGYKDLBEGDLADVA 600  
QY 601 VGASQMIIVLSSRPVDMVTLMSPSPARIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
DB 601 VGASQMIIVLSSRPVDMVTLMSPSPARIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
QY 661 POFQGRVLANLTYTLQLDGHRTRRRGLFPGGRHELRNIAVTTSMSCDTSFHFVVCQD 720



Db 661 POFGRIVANLTYTLQLDGHRTRRGLFPGRHELRNIAVTTSMSCDTSFHFVVCVD 720  
Qy 721 LISPIVNSLNFSLMEEBGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGDKCEAN 780  
Db 721 LISPIVNSLNFSLMEEBGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGDKCEAN 780  
Qy 781 LRVSPSPARARLRLTAFAASLVELSLNLEBDAYWQDLHFPGLSPFRKVEMLKPHSQ 840  
Db 781 LRVSPSPARARLRLTAFAASLVELSLNLEBDAYWQDLHFPGLSPFRKVEMLKPHSQ 840  
Qy 841 IPVCEELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSGDSVELHANVTC 900  
Db 841 IPVCEELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSGDSVELHANVTC 900  
Qy 901 NNEBSDLLEDSATTTIPIILYPINILIQDQEDSTLYVSFTPKGPKIHQVKMYQVRIOPS 960  
Db 901 NNEBSDLLEDSATTTIPIILYPINILIQDQEDSTLYVSFTPKGPKIHQVKMYQVRIOPS 960  
Qy 961 IHDNIPITLVAVGVPPPSBGPITHQMSVQMEPPVPCHEDELERLPAAEPCLPGLALFR 1020  
Db 961 IHDNIPITLVAVGVPPPSBGPITHQMSVQMEPPVPCHEDELERLPAAEPCLPGLALFR 1020  
Qy 1021 CPVVFROEILVQVIGTLELVEGEIEASSMFSLSLCSLSISFNSSKHPLHLYGSNASLAQVVMK 1080  
Db 1021 CPVVFROEILVQVIGTLELVEGEIEASSMFSLSLCSLSISFNSSKHPLHLYGSNASLAQVVMK 1080  
Qy 1081 VDVIYKQMLLYLVLSGIGGLLLLLLIPIVLYKVGFFPKRNLKEKMEAGRGVNGIPIADS 1140  
Db 1081 VDVIYKQMLLYLVLSGIGGLLLLLLIPIVLYKVGFFPKRNLKEKMEAGRGVNGIPIADS 1140  
Qy 1141 EQLASGQAGDPGCLKPLHEKDSGSGGKD 1170  
Db 1141 EQLASGQAGDPGCLKPLHEKDSGSGGKD 1170

RESULT 12  
US-09-791-537-118794  
; Sequence 118794; Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biocomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 118794  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-118794

Query Match 99.9%; Score 6098; DB 22; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCTIVAMALLSGFFFAPASSYNLDVGAASFPPRAGRHRHGYVLQVANGVTVGA 60  
Db 1 MKDSCTIVAMALLSGFFFAPASSYNLDVGAASFPPRAGRHRHGYVLQVANGVTVGA 60  
Qy 61 PGBENSTSLYQCGSGTHCLPVTLRGSNTSKYLGMTLADPTDGSLLACDPGLSRTCD 120  
Db 61 PGBENSTSLYQCGSGTHCLPVTLRGSNTSKYLGMTLADPTDGSLLACDPGLSRTCD 120  
Qy 61 PGBENSTSLYQCGSGTHCLPVTLRGSNTSKYLGMTLADPTDGSLLACDPGLSRTCD 120  
Db 61 PGBENSTSLYQCGSGTHCLPVTLRGSNTSKYLGMTLADPTDGSLLACDPGLSRTCD 120  
Qy 121 QNTYLSGLCYLFRQMLQSPMLQGRPGFOBCIKGNVDLFLFDGSMSLQPDFOKILDPMK 180  
Db 121 QNTYLSGLCYLFRQMLQSPMLQGRPGFOBCIKGNVDLFLFDGSMSLQPDFOKILDPMK 180  
Qy 181 DVMKGLSNTSYQFAAVOPSTSYKTEFDPDSDYVKRDPALLKHVGMULLTNTFGAINVY 240

Db 181 DVMKGLSNTSYQFAAVOPSTSYKTEFDPDSDYVKRDPALLKHVGMULLTNTFGAINVY 240  
Qy 241 ATEVFRRELGARPATVLLIITDGEATDSCNIDAAODIIRYIIGIKHQTESQETLH 300  
Db 241 ATEVFRRELGARPATVLLIITDGEATDSCNIDAAODIIRYIIGIKHQTESQETLH 300  
Qy 301 KFASKPASEFVKIITDEKLDLFTTELQKKIYYIEGTSKODLTSFNNELSSSGISADLSR 360  
Db 301 KFASKPASEFVKIITDEKLDLFTTELQKKIYYIEGTSKODLTSFNNELSSSGISADLSR 360  
Qy 361 GHAVAVGAKDWAAGFLDKADLQDDTFIGNBPLTEVAVAGLYGYVTWLPSRQKTSLL 420  
Db 361 GHAVAVGAKDWAAGFLDKADLQDDTFIGNBPLTEVAVAGLYGYVTWLPSRQKTSLL 420  
Qy 421 ASGARVQHMGRVLLPQEPQGGHMSQVOTIHGTQIGSYFGELCGVDVQDGETELLII 480  
Db 421 ASGARVQHMGRVLLPQEPQGGHMSQVOTIHGTQIGSYFGELCGVDVQDGETELLII 480  
Qy 481 GAPLFYGEORGGRVFIYQRRQLGFEBYSBLQGPBGYPFAGFGEATLALTDINGDLVDA 540  
Db 481 GAPLFYGEORGGRVFIYQRRQLGFEBYSBLQGPBGYPFAGFGEATLALTDINGDLVDA 540  
Qy 541 VGABLEQAGAVYIFNGRHGGLSPQSRIEGTQVLSGIQMPGSGIHGVKDLBGDLADVA 600  
Db 541 VGABLEQAGAVYIFNGRHGGLSPQSRIEGTQVLSGIQMPGSGIHGVKDLBGDLADVA 600  
Qy 601 VGASQOIVLSSRRVDMVMTLMSFPAEIPVHEGCSYTSNKKKEBVTITICQIKSLY 660  
Db 601 VGASQOIVLSSRRVDMVMTLMSFPAEIPVHEGCSYTSNKKKEBVTITICQIKSLY 660  
Qy 661 POFGRIVANLTYTLQLDGHRTRRGLFPGRHELRNIAVTTSMSCDTSFHFVVCVD 720  
Db 661 POFGRIVANLTYTLQLDGHRTRRGLFPGRHELRNIAVTTSMSCDTSFHFVVCVD 720  
Qy 721 LISPIVNSLNFSLMEEBGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGDKCEAN 780  
Db 721 LISPIVNSLNFSLMEEBGTPRDQRAQKDIPIILRPSLHSETWEIPEKNGGDKCEAN 780  
Qy 781 LRVSPSPARARLRLTAFAASLVELSLNLEBDAYWQDLHFPGLSPFRKVEMLKPHSQ 840  
Db 781 LRVSPSPARARLRLTAFAASLVELSLNLEBDAYWQDLHFPGLSPFRKVEMLKPHSQ 840  
Qy 841 IPVCEELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSGDSVELHANVTC 900  
Db 841 IPVCEELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSGDSVELHANVTC 900  
Qy 901 NNEBSDLLEDSATTTIPIILYPINILIQDQEDSTLYVSFTPKGPKIHQVKMYQVRIOPS 960  
Db 901 NNEBSDLLEDSATTTIPIILYPINILIQDQEDSTLYVSFTPKGPKIHQVKMYQVRIOPS 960  
Qy 961 IHDNIPITLVAVGVPPPSBGPITHQMSVQMEPPVPCHEDELERLPAAEPCLPGLALFR 1020  
Db 961 IHDNIPITLVAVGVPPPSBGPITHQMSVQMEPPVPCHEDELERLPAAEPCLPGLALFR 1020  
Qy 1021 CPVVFROEILVQVIGTLELVEGEIEASSMFSLSLCSLSISFNSSKHPLHLYGSNASLAQVVMK 1080  
Db 1021 CPVVFROEILVQVIGTLELVEGEIEASSMFSLSLCSLSISFNSSKHPLHLYGSNASLAQVVMK 1080  
Qy 1081 VDVIYKQMLLYLVLSGIGGLLLLLLIPIVLYKVGFFPKRNLKEKMEAGRGVNGIPIADS 1140  
Db 1081 VDVIYKQMLLYLVLSGIGGLLLLLLIPIVLYKVGFFPKRNLKEKMEAGRGVNGIPIADS 1140  
Qy 1141 EQLASGQAGDPGCLKPLHEKDSGSGGKD 1170  
Db 1141 EQLASGQAGDPGCLKPLHEKDSGSGGKD 1170

RESULT 13  
US-10-170-205B-35754  
; Sequence 35754; Application US/10170205E  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, Mark



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; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: C1001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35754
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-35754

Query Match      99.9%; Score 6098; DB 27; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGARSPFPAGRHFGYRVLYQVNGVYVGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGARSPFPAGRHFGYRVLYQVNGVYVGA 60
QY 61 PGBNGSTSLYQCQSGTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
DB 61 PGBNGSTSLYQCQSGTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDLVFLPDGSMISLOPDEFQKILDFMK 180
DB 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDLVFLPDGSMISLOPDEFQKILDFMK 180
QY 181 DVMKCLNTSYQFAVQSTSYKTEPDSYVKRDPALLKHVGMILLTNTFGAINVY 240
DB 181 DVMKCLNTSYQFAVQSTSYKTEPDSYVKRDPALLKHVGMILLTNTFGAINVY 240
QY 241 ATBVRREELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
DB 241 ATBVRREELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
QY 301 KFAKSPASEFVKILDFTEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360
DB 301 KFAKSPASEFVKILDFTEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360
QY 361 GHAVVGAAGAKDMAGGLDLKADLDDPTFIGNBFLTPVRAGYLYVTWMLPSRKSTSL 420
DB 361 GHAVVGAAGAKDMAGGLDLKADLDDPTFIGNBFLTPVRAGYLYVTWMLPSRKSTSL 420
QY 421 ASDAPRYQHMGRVLLFQEPQGGHMSQYQTIHGTOIGSYFGGELCGVVDODGETELLII 480
DB 421 ASDAPRYQHMGRVLLFQEPQGGHMSQYQTIHGTOIGSYFGGELCGVVDODGETELLII 480
QY 481 GAPLFYGEORGGRVFIYORRQLGFEEVESELQDPEGYPLGRFGEAITALTINDGGLVDVA 540
DB 481 GAPLFYGEORGGRVFIYORRQLGFEEVESELQDPEGYPLGRFGEAITALTINDGGLVDVA 540
QY 541 VGAPLEEGGAYYIFNGRHGGLSPQPSORIEGTQVLSGIQWFGRSIHGKDLBGLDAVYA 600
DB 541 VGAPLEEGGAYYIFNGRHGGLSPQPSORIEGTQVLSGIQWFGRSIHGKDLBGLDAVYA 600
QY 601 VGASEQMTVLSRPVVDWVTLMSPSPAIPIVHEVCSYSTSNKMEGVNITICFOIKSLY 660
DB 601 VGASEQMTVLSRPVVDWVTLMSPSPAIPIVHEVCSYSTSNKMEGVNITICFOIKSLY 660
QY 661 POFOGRVLAANTLYTLQLDGHTRRRGLPFGGHEILRRNIATVTSMSCTDFSHPFVQVD 720
DB 661 POFOGRVLAANTLYTLQLDGHTRRRGLPFGGHEILRRNIATVTSMSCTDFSHPFVQVD 720
QY 721 LIISPINVLNFSIMEEGTPRDORAGKDIPRIILPSLSHETWEIIPKKNCGEDKCCAN 780
DB 721 LIISPINVLNFSIMEEGTPRDORAGKDIPRIILPSLSHETWEIIPKKNCGEDKCCAN 780
QY 781 LRVSPSPASRALRLTAFAASLVELSLSANLEDAVWVOLDLHFPGLSPFRKVMKLPKPSQ 840
DB 781 LRVSPSPASRALRLTAFAASLVELSLSANLEDAVWVOLDLHFPGLSPFRKVMKLPKPSQ 840
QY 840 LRVSPSPASRALRLTAFAASLVELSLSANLEDAVWVOLDLHFPGLSPFRKVMKLPKPSQ 840
DB 840 LRVSPSPASRALRLTAFAASLVELSLSANLEDAVWVOLDLHFPGLSPFRKVMKLPKPSQ 840
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QY 841 IPVSCBELPEERSRLLSRASCNVSPPIFKASHVALQWMENTLYNNSGSDVELHANVTC 900
DB 841 IPVSCBELPEERSRLLSRASCNVSPPIFKASHVALQWMENTLYNNSGSDVELHANVTC 900
QY 901 NNEBSDLLEDSNATTTIPIILPINILIODDESTLYSFTFKGPKIHQVKMYQVRLOPS 960
DB 901 NNEBSDLLEDSNATTTIPIILPINILIODDESTLYSFTFKGPKIHQVKMYQVRLOPS 960
QY 961 IHDNIPITLNAVGVPOPPSEGPITTHQMSVQMEPPVPCHEYDLRLPDAAEPCLPGLALFR 1020
DB 961 IHDNIPITLNAVGVPOPPSEGPITTHQMSVQMEPPVPCHEYDLRLPDAAEPCLPGLALFR 1020
QY 1021 CPVVRROEILVQVGTLELVEIEIASMFSICSSLSISFNSKXPHLYGSNALSIAQVVMK 1080
DB 1021 CPVVRROEILVQVGTLELVEIEIASMFSICSSLSISFNSKXPHLYGSNALSIAQVVMK 1080
QY 1081 DVVYERQMTLYLVLSGIGILLILLIFIVLYKKGFFPRNKKEMEAGRGVPMGI PAEDS 1140
DB 1081 DVVYERQMTLYLVLSGIGILLILLIFIVLYKKGFFPRNKKEMEAGRGVPMGI PAEDS 1140
QY 1141 EQLASQDAGDPGCLKPLHEKDSSESGGKD 1170
DB 1141 EQLASQDAGDPGCLKPLHEKDSSESGGKD 1170

RESULT 14
US-10-261-164-1
; Sequence 1, Application US/10261164
; GENERAL INFORMATION:
; APPLICANT: KAPUSTAV, PAMELA M.
; TITLE OF INVENTION: LFA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: 046007/0272304
; CURRENT APPLICATION NUMBER: US/10/261,164
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-164-1

Query Match      99.9%; Score 6098; DB 28; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGARSPFPAGRHFGYRVLYQVNGVYVGA 60
DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVKGARSPFPAGRHFGYRVLYQVNGVYVGA 60
QY 61 PGBNGSTSLYQCQSGTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
DB 61 PGBNGSTSLYQCQSGTGHCPLVTLRGSNTYSKYLGMTLATDPTDGSILACDPGLSRTCD 120
QY 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDLVFLPDGSMISLOPDEFQKILDFMK 180
DB 121 QNTYLSGLCYLFRONTLQGPMLQGRPGFOECIKGNVDLVFLPDGSMISLOPDEFQKILDFMK 180
QY 181 DVMKCLNTSYQFAVQSTSYKTEPDSYVKRDPALLKHVGMILLTNTFGAINVY 240
DB 181 DVMKCLNTSYQFAVQSTSYKTEPDSYVKRDPALLKHVGMILLTNTFGAINVY 240
QY 241 ATBVRREELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
DB 241 ATBVRREELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIGHFQTKESQETLH 300
QY 301 KFAKSPASEFVKILDFTEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360
DB 301 KFAKSPASEFVKILDFTEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSSGISADLSR 360
QY 361 GHAVVGAAGAKDMAGGLDLKADLDDPTFIGNBFLTPVRAGYLYVTWMLPSRKSTSL 420
DB 361 GHAVVGAAGAKDMAGGLDLKADLDDPTFIGNBFLTPVRAGYLYVTWMLPSRKSTSL 420
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Db 361 GHAVVAVGAKDMAGFLDLKADLDDPTFIGNBPLTEPRVAGYLGVTWMLPSROKTSLL 420
Qy 421 ASGAPRYOHMGRRVLLFQEPGGGHSQVOTIHGTIGSYFGGELCGVDDODGETELLII 480
Db 421 ASGAPRYOHMGRRVLLFQEPGGGHSQVOTIHGTIGSYFGGELCGVDDODGETELLII 480
Qy 481 GAPLFYEGORGRVFIYQRRQLGFEVESELQDPCGYPLGRFGAITALTDINDGLVDVA 540
Db 481 GAPLFYEGORGRVFIYQRRQLGFEVESELQDPCGYPLGRFGAITALTDINDGLVDVA 540
Qy 541 VGAPLEEGAVYIFNGRHGGLSPQPSQRIEQTUYSGLQMFGRSHGVKDLBEGDLADVA 600
Db 541 VGAPLEEGAVYIFNGRHGGLSPQPSQRIEQTUYSGLQMFGRSHGVKDLBEGDLADVA 600
Qy 601 VGASOMIVLSSRPVDMVTLMSPFAIPVHEVCSYSTSNKMEGVNITTCPOIKSLY 660
Db 601 VGASOMIVLSSRPVDMVTLMSPFAIPVHEVCSYSTSNKMEGVNITTCPOIKSLY 660
Qy 661 POFQGRIVANLTYTLQDGHRTRRRGLPGRGHELRNIAVTTSMSCTDPSFHPVCVOD 720
Db 661 POFQGRIVANLTYTLQDGHRTRRRGLPGRGHELRNIAVTTSMSCTDPSFHPVCVOD 720
Qy 721 LISPIVNSLNFSLMBEESTPRDQRAQKDIPIILRPSLHSETWEIPFEKNGCEDKKEAN 780
Db 721 LISPIVNSLNFSLMBEESTPRDQRAQKDIPIILRPSLHSETWEIPFEKNGCEDKKEAN 780
Qy 781 LRVFSFARSARALRLTAPASLVELSLSNLEDAVWVOLDLHPPGSLFRKVEMLKPHSQ 840
Db 781 LRVFSFARSARALRLTAPASLVELSLSNLEDAVWVOLDLHPPGSLFRKVEMLKPHSQ 840
Qy 841 IPVSCBELPESRLLSRALSCNVSSPIFKAGSHVALQMMFNTLVNSWGDSEVELHANVTC 900
Db 841 IPVSCBELPESRLLSRALSCNVSSPIFKAGSHVALQMMFNTLVNSWGDSEVELHANVTC 900
Qy 901 NNEBSDLLEDSATITIIPIILPINLIDQDSDSTLYSFTPKGPIHGVKMYQVRIOPS 960
Db 901 NNEBSDLLEDSATITIIPIILPINLIDQDSDSTLYSFTPKGPIHGVKMYQVRIOPS 960
Qy 961 IHDNIPILBAVGVOPPSGPIITHOMSVOMEPVPVCHYEDLELPPAAEPCLPGALFR 1020
Db 961 IHDNIPILBAVGVOPPSGPIITHOMSVOMEPVPVCHYEDLELPPAAEPCLPGALFR 1020
Qy 1021 CPVFEROELIYOVTGTELVGEIEASMSFSLCSLSISFNSSKHEHLVGSNLSLAQVVMK 1080
Db 1021 CPVFEROELIYOVTGTELVGEIEASMSFSLCSLSISFNSSKHEHLVGSNLSLAQVVMK 1080
Qy 1081 VDVIYKEMMLTYLVSIGIGILLLLIPIYVYKGFPRKNIKEMEAGRGVPMGIPADS 1140
Db 1081 VDVIYKEMMLTYLVSIGIGILLLLIPIYVYKGFPRKNIKEMEAGRGVPMGIPADS 1140
Qy 1141 EQLASGOEADPGCLKPLHEKDSBSGGKD 1170
Db 1141 EQLASGOEADPGCLKPLHEKDSBSGGKD 1170

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; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 9966
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9350
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-325-899-9350

Query Match      99.9%; Score 6098; DB 29; Length 1170;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVMALLSGFFFPAPASVYLDVRGARSFEPAPAGRHFGRYLVQVNGVYVGA 60
Db 1 MKDSCITVMALLSGFFFPAPASVYLDVRGARSFEPAPAGRHFGRYLVQVNGVYVGA 60
Qy 61 PEGNSSTGSLYQCSGTGHCPLYLRGNSYTSKYLQMTLATDPTDGSILA CDPGLSRTCD 120
Db 61 PEGNSSTGSLYQCSGTGHCPLYLRGNSYTSKYLQMTLATDPTDGSILA CDPGLSRTCD 120
Qy 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFQECIKANVDLVFLPDSMSLQDPEFKILDFMK 180
Db 121 QNTYLSGLCYLFRQNLQGPMLQGRPGFQECIKANVDLVFLPDSMSLQDPEFKILDFMK 180
Qy 181 DVMKLSNTSYQFAAVQFSTSYKTEFPDSDYVRKDPDALIKKVKHMLLTNTFGAIVNV 240
Db 181 DVMKLSNTSYQFAAVQFSTSYKTEFPDSDYVRKDPDALIKKVKHMLLTNTFGAIVNV 240
Qy 241 ATEVFREELGAPDPAATVLIITDGEATDSGNIDAANDIIRYIIGIKHFQYKESQETLH 300
Db 241 ATEVFREELGAPDPAATVLIITDGEATDSGNIDAANDIIRYIIGIKHFQYKESQETLH 300
Qy 301 KEASKPASEFVKILDPFEKIKDLFTBELQKIIYVIEGSKODLTSFNNESSSGISADLSR 360
Db 301 KEASKPASEFVKILDPFEKIKDLFTBELQKIIYVIEGSKODLTSFNNESSSGISADLSR 360
Qy 361 GHAVVAVGAKDMAGFLDLKADLDDPTFIGNBPLTEPRVAGYLGVTWMLPSROKTSLL 420
Db 361 GHAVVAVGAKDMAGFLDLKADLDDPTFIGNBPLTEPRVAGYLGVTWMLPSROKTSLL 420
Qy 421 ASGAPRYOHMGRRVLLFQEPGGGHSQVOTIHGTIGSYFGGELCGVDDODGETELLII 480
Db 421 ASGAPRYOHMGRRVLLFQEPGGGHSQVOTIHGTIGSYFGGELCGVDDODGETELLII 480
Qy 481 GAPLFYEGORGRVFIYQRRQLGFEVESELQDPCGYPLGRFGAITALTDINDGLVDVA 540
Db 481 GAPLFYEGORGRVFIYQRRQLGFEVESELQDPCGYPLGRFGAITALTDINDGLVDVA 540
Qy 541 VGAPLEEGAVYIFNGRHGGLSPQPSQRIEQTUYSGLQMFGRSHGVKDLBEGDLADVA 600
Db 541 VGAPLEEGAVYIFNGRHGGLSPQPSQRIEQTUYSGLQMFGRSHGVKDLBEGDLADVA 600
Qy 601 VGASOMIVLSSRPVDMVTLMSPFAIPVHEVCSYSTSNKMEGVNITTCPOIKSLY 660
Db 601 VGASOMIVLSSRPVDMVTLMSPFAIPVHEVCSYSTSNKMEGVNITTCPOIKSLY 660
Qy 661 POFQGRIVANLTYTLQDGHRTRRRGLPGRGHELRNIAVTTSMSCTDPSFHPVCVOD 720
Db 661 POFQGRIVANLTYTLQDGHRTRRRGLPGRGHELRNIAVTTSMSCTDPSFHPVCVOD 720
Qy 721 LISPIVNSLNFSLMBEESTPRDQRAQKDIPIILRPSLHSETWEIPFEKNGCEDKKEAN 780
Db 721 LISPIVNSLNFSLMBEESTPRDQRAQKDIPIILRPSLHSETWEIPFEKNGCEDKKEAN 780
Qy 781 LRVFSFARSARALRLTAPASLVELSLSNLEDAVWVOLDLHPPGSLFRKVEMLKPHSQ 840
Db 781 LRVFSFARSARALRLTAPASLVELSLSNLEDAVWVOLDLHPPGSLFRKVEMLKPHSQ 840
Qy 841 IPVSCBELPESRLLSRALSCNVSSPIFKAGSHVALQMMFNTLVNSWGDSEVELHANVTC 900
Db 841 IPVSCBELPESRLLSRALSCNVSSPIFKAGSHVALQMMFNTLVNSWGDSEVELHANVTC 900

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# RESULT 15

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US-10-325-899-9350
; Sequence 9350, Application US/10325899
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
; TITLE OF INVENTION: REJECTION
; FILE REFERENCE: 506612000122
; CURRENT FILING DATE: 2002-12-20
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/131,831

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Qy	901	NNEDSDLEDNSATTIIPILYPINILIOEDSTLYSFTPKPKIHQKMYQVRIQPS	960
Db	901	NNEDSDLEDNSATTIIPILYPINILIOEDSTLYSFTPKPKIHQKMYQVRIQPS	960
Qy	961	IHDHNIPTLEAVGVGPSPSEGPITHQNSVQMEPPVPCHYEDLERLPDAEPCLEPGLFR	1020
Db	961	IHDHNIPTLEAVGVGPSPSEGPITHQNSVQMEPPVPCHYEDLERLPDAEPCLEPGLFR	1020
Qy	1021	CPVVRROELIVQVIGTLELVGEIEASSMFSICSSISIFNSGKHFLYGSNASTLAQVYMK	1080
Db	1021	CPVVRROELIVQVIGTLELVGEIEASSMFSICSSISIFNSGKHFLYGSNASTLAQVYMK	1080
Qy	1081	VDVYVEKQMLYLYVLSGIGLLLLIFLYLYKVGFPKRNLEKMEAGRGVNGIPEADS	1140
Db	1081	VDVYVEKQMLYLYVLSGIGLLLLIFLYLYKVGFPKRNLEKMEAGRGVNGIPEADS	1140
Qy	1141	EQLASGQEAQDPCGCKPLHEKDSGSGGKD	1170
Db	1141	EQLASGQEAQDPCGCKPLHEKDSGSGGKD	1170

Search completed: August 29, 2005, 19:35:37  
 Job time : 489 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: August 29, 2005, 19:21:54 ; Search time 86 Seconds

(without alignments)  
2139.235 Million cell updates/sec

Title: US-09-945-265-2

Perfect score: 6106  
Sequence: 1 MKDSCITVMAMALLSGFFFF.....DPGLKPLHEDSSGGKGD 1170

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 729853 seqs, 15724287 residues

Total number of hits satisfying chosen parameters: 729853

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New:\*

- 1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*
- 7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep:\*
- 8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6106	100.0	1170	1 PCT-US05-02350-142	Sequence 142, App
2	6106	100.0	1170	7 US-11-043-770-142	Sequence 142, App
3	6106	100.0	1170	7 US-11-080-026-2	Sequence 2, Appli
4	6106	100.0	1170	7 US-11-107-028-4	Sequence 4, Appli
5	6098	99.9	1170	1 PCT-US05-02350-653	Sequence 653, App
6	6098	99.9	1170	5 US-09-976-935A-36	Sequence 36, Appl
7	6098	99.9	1170	7 US-11-043-770-653	Sequence 653, App
8	6098	99.9	1170	7 US-11-062-290-1	Sequence 1, Appli
9	6053.5	99.1	1223	1 PCT-US03-10870-295	Sequence 295, App
10	5981	98.0	1145	7 US-11-021-951-130	Sequence 130, App
11	5585	91.5	1086	1 PCT-US03-10870-1871	Sequence 1871, App
12	3885	63.6	750	1 PCT-US05-02350-80	Sequence 80, Appl
13	3885	63.6	750	7 US-11-043-770-80	Sequence 80, Appl
14	3066	50.2	589	7 US-11-062-290-2	Sequence 2, Appli
15	1564	25.6	1154	8 US-60-651-235-76	Sequence 76, Appl
16	1564	25.6	1154	8 US-60-680-004-144	Sequence 144, App
17	1564	25.6	1154	8 US-60-701-054-258	Sequence 258, App
18	1563.5	25.6	1152	8 US-60-651-235-74	Sequence 74, Appl
19	1563.5	25.6	1152	8 US-60-651-235-77	Sequence 77, Appl
20	1563.5	25.6	1153	8 US-60-680-004-145	Sequence 145, App
21	1563.5	25.6	1153	8 US-60-701-054-259	Sequence 259, App
22	1562.5	25.6	1152	1 PCT-US05-02350-141	Sequence 141, App
23	1562.5	25.6	1152	7 US-11-043-770-141	Sequence 141, App
24	1562.5	25.6	1152	7 US-11-080-026-4	Sequence 4, Appli
25	1562.5	25.6	1152	8 US-60-651-235-75	Sequence 75, Appli

26	1562.5	25.6	1152	8 US-60-680-004-143	Sequence 143, App
27	1562.5	25.6	1152	8 US-60-701-054-257	Sequence 257, App
28	1154.5	18.9	1217	6 US-10-940-774A-7892	Sequence 7892, App
29	1154	18.9	1189	6 US-10-450-763-43308	Sequence 43308, A
30	1149.5	18.8	1188	7 US-11-175-714-147	Sequence 147, App
31	1146.5	18.8	1188	5 US-09-980-403A-2	Sequence 2, Appli
32	1139	18.7	1166	7 US-11-175-714-148	Sequence 148, App
33	1132	18.4	1188	7 US-11-175-714-165	Sequence 165, App
34	1121.5	18.4	1177	8 US-60-664-611-976	Sequence 976, App
35	1121.5	18.4	1177	8 US-60-664-936-459	Sequence 459, App
36	1121.5	18.4	1178	7 US-11-154-939-951	Sequence 951, App
37	1121.5	18.4	1178	7 US-11-167-575-951	Sequence 951, App
38	1121.5	18.4	1178	8 US-60-679-970-847	Sequence 847, App
39	1121.5	18.4	1178	8 US-60-680-002-508	Sequence 508, App
40	1117.5	18.3	1179	7 US-11-154-939-950	Sequence 950, App
41	1117.5	18.3	1179	7 US-11-167-575-950	Sequence 950, App
42	1117.5	18.3	1179	8 US-60-664-611-975	Sequence 975, App
43	1117.5	18.3	1179	8 US-60-664-936-458	Sequence 458, App
44	1117.5	18.3	1179	8 US-60-679-970-843	Sequence 843, App
45	1117.5	18.3	1179	8 US-60-680-002-504	Sequence 504, App

ALIGNMENTS

RESULT 1  
PCT-US05-02350-142  
Sequence 142, Application PC/TUS0502350  
GENERAL INFORMATION:  
APPLICANT: Ayalon-Soffer, Michal  
APPLICANT: Levine, Zurit  
APPLICANT: Sella-Tavor, Osnat  
APPLICANT: Diber, Alex  
APPLICANT: Shemesh, Ronen  
APPLICANT: Toporik, Amir  
APPLICANT: Rotman, Galit  
APPLICANT: Nemzer, Sergey  
APPLICANT: Rosenberg, Avi  
APPLICANT: Dahan, Dvir  
APPLICANT: Wool, Asaf  
APPLICANT: Cojocaru, Gad S.  
APPLICANT: Aktva, Plinchas  
APPLICANT: Pollock, Sarah  
APPLICANT: Savitsky, Kineret  
APPLICANT: Bernstein, Jeanne  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
FILE REFERENCE: 28487  
CURRENT APPLICATION NUMBER: PCT/US05/02350  
CURRENT FILING DATE: 2005-02-10  
NUMBER OF SEQ ID NOS: 1155  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 142  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US05-02350-142  
Query Match 100.0%; Score 6106; DB 1; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCITVMAMALLSGFFFPAPASSYMLDVRGARSFSPRAGRHFGRVIVGVGVYGA 60  
DB 1 MKDSCITVMAMALLSGFFFPAPASSYMLDVRGARSFSPRAGRHFGRVIVGVGVYGA 60  
QY PGEAGNSGSLYQCCSGGHCIPVTLRGSNTSKYLTATDPDGSILACDPGLSTRCD 120  
DB PGEAGNSGSLYQCCSGGHCIPVTLRGSNTSKYLTATDPDGSILACDPGLSTRCD 120  
QY QNTYLSGICVLFRLNQLGPMLOGRPFQECIKGNVDLVFLPDGSMISLPDEFQKILDFMK 180  
DB QNTYLSGICVLFRLNQLGPMLOGRPFQECIKGNVDLVFLPDGSMISLPDEFQKILDFMK 180

QY 181 DVMKLSNTSYQFAVQFSTSYKTEFPDSYVKRDPALLKHYKMLLNTFGAINVY 240  
DB 181 DVMKLSNTSYQFAVQFSTSYKTEFPDSYVKRDPALLKHYKMLLNTFGAINVY 240  
QY 241 ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIKHPQTKESQETLH 300  
DB 241 ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIKHPQTKESQETLH 300  
QY 301 KFASKPASEFVKIIDTEPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSGISADLSR 360  
DB 301 KFASKPASEFVKIIDTEPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSGISADLSR 360  
QY 361 GHAVVAGVAKDMAAGFLDLKADLQDDPTFIGNEBLPEVRAGYGYVTWMLPSRQKTSLL 420  
DB 361 GHAVVAGVAKDMAAGFLDLKADLQDDPTFIGNEBLPEVRAGYGYVTWMLPSRQKTSLL 420  
QY 421 ASGAPRYQHMGRVLLFQEPQGGGHSQVQTHGTQIGSYFGGELCGVDVDDGTELLLI 480  
DB 421 ASGAPRYQHMGRVLLFQEPQGGGHSQVQTHGTQIGSYFGGELCGVDVDDGTELLLI 480  
QY 481 GAPLFYGEORGRVFIYORROLGFEVSELQDPCGYLGRFGAETALTIDINGGLVDA 540  
DB 481 GAPLFYGEORGRVFIYORROLGFEVSELQDPCGYLGRFGAETALTIDINGGLVDA 540  
QY 541 VGAPLEBQAVYIFNGRHGGLSPQPSQRIEGTOVLSGIQWFGRSIHGVKDEBGLADVA 600  
DB 541 VGAPLEBQAVYIFNGRHGGLSPQPSQRIEGTOVLSGIQWFGRSIHGVKDEBGLADVA 600  
QY 601 VGASQOMTVLSSRPVDMVTLMSPBAIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
DB 601 VGASQOMTVLSSRPVDMVTLMSPBAIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
QY 661 POFQGRVANTLYTLQDLGHRTRRGLPFGGRHLEARNIAVTTSMCTDPSFHPVCQD 720  
DB 661 POFQGRVANTLYTLQDLGHRTRRGLPFGGRHLEARNIAVTTSMCTDPSFHPVCQD 720  
QY 721 LISPINVSLNLSMBEETPRDQAOQKODIPILRPSLHSETWEIPEKNGCEDKCBAN 780  
DB 721 LISPINVSLNLSMBEETPRDQAOQKODIPILRPSLHSETWEIPEKNGCEDKCBAN 780  
QY 781 LRVFSPSPARALRLTAFASLSVELSLNLEBDATWQDLHFPGLSFRKVEMLKPHSQ 840  
DB 781 LRVFSPSPARALRLTAFASLSVELSLNLEBDATWQDLHFPGLSFRKVEMLKPHSQ 840  
QY 841 IPVSCBELPEESRLSLRASCNVSSPIFKAGHSVALQMMFNTLVNSSWGDSEVLEHANTC 900  
DB 841 IPVSCBELPEESRLSLRASCNVSSPIFKAGHSVALQMMFNTLVNSSWGDSEVLEHANTC 900  
QY 901 NNEBSDLLEDSATTTIPIILYPINILQDQDSTLYSFTPKGPKIHQVKMYQVRIQPS 960  
DB 901 NNEBSDLLEDSATTTIPIILYPINILQDQDSTLYSFTPKGPKIHQVKMYQVRIQPS 960  
QY 961 IHDNIPITLNAVGVPOPPSEGPITTHQMSVQMEPPVPCHEYDLERLPDAAPCPLGALFR 1020  
DB 961 IHDNIPITLNAVGVPOPPSEGPITTHQMSVQMEPPVPCHEYDLERLPDAAPCPLGALFR 1020  
QY 1021 CPVVFROGIIIVOGITLVEIGETIASSMFSLCSSLISFNSSKPHLYGSMASLAQVVMK 1080  
DB 1021 CPVVFROGIIIVOGITLVEIGETIASSMFSLCSSLISFNSSKPHLYGSMASLAQVVMK 1080  
QY 1081 VDVIYKQKMLLYLVLSGIGLILLLLIIFIVLYKVFGRNLKXKMEAGRGVNGIAPADS 1140  
DB 1081 VDVIYKQKMLLYLVLSGIGLILLLLIIFIVLYKVFGRNLKXKMEAGRGVNGIAPADS 1140  
QY 1141 EQLASGQEAQDPCCLPKLHEKDSBGSGKD 1170  
DB 1141 EQLASGQEAQDPCCLPKLHEKDSBGSGKD 1170

RESULT 2

US-11-043-770-142

; Sequence 142; Application US/11043770

GENERAL INFORMATION:  
APPLICANT: Ayalon-Soffer, Michael  
APPLICANT: Levine, Zurit  
APPLICANT: Sella-Tavor, Osnat  
APPLICANT: Diber, Alex  
APPLICANT: Shemesh, Ronen  
APPLICANT: Toporik, Amir  
APPLICANT: Rotman, Galit  
APPLICANT: Nemzer, Sergey  
APPLICANT: Rosenberg, Avi  
APPLICANT: Danary, Dvir  
APPLICANT: Wool, Assaf  
APPLICANT: Cojocaru, Gad S.  
APPLICANT: Akiva, Pinchas  
APPLICANT: Pollock, Sarah  
APPLICANT: Savitsky, Kimeret  
APPLICANT: Bernstein, Jeanne  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
FILE REFERENCE: 28486  
CURRENT APPLICATION NUMBER: US/11/043, 770  
NUMBER OF SEQ ID NOS: 1155  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 142  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-043-770-142

Query Match 100.0%; Score 6106; DB 7; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKOSCTVMAALLSGFFPAPASNYLDVRGARSFPPAPGRHGRVYQVNGVYVGA 60  
QY 61 PGBNSTGSLYOCOSGCHCLPVTLRGNTSKYLGMTLATDPPDGSIIACDPGLSRTCD 120  
DB 61 PGBNSTGSLYOCOSGCHCLPVTLRGNTSKYLGMTLATDPPDGSIIACDPGLSRTCD 120  
QY 121 QNTYLSGLCYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLPDSMSLOPDEFOKILDFMK 180  
DB 121 QNTYLSGLCYLFRONTLOGPMLQGRPGFQECIKGNVDLVFLPDSMSLOPDEFOKILDFMK 180  
QY 181 DVMKLSNTSYQFAVQFSTSYKTEFPDSYVKRDPALLKHYKMLLNTFGAINVY 240  
DB 181 DVMKLSNTSYQFAVQFSTSYKTEFPDSYVKRDPALLKHYKMLLNTFGAINVY 240  
QY 241 ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIKHPQTKESQETLH 300  
DB 241 ATEVFEELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIKHPQTKESQETLH 300  
QY 301 KFASKPASEFVKIIDTEPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSGISADLSR 360  
DB 301 KFASKPASEFVKIIDTEPEKLDLFTLEOKKIYVIEGTSKODLTSFNMELSSGISADLSR 360  
QY 361 GHAVVAGVAKDMAAGFLDLKADLQDDPTFIGNEBLPEVRAGYGYVTWMLPSRQKTSLL 420  
DB 361 GHAVVAGVAKDMAAGFLDLKADLQDDPTFIGNEBLPEVRAGYGYVTWMLPSRQKTSLL 420  
QY 421 ASGAPRYQHMGRVLLFQEPQGGGHSQVQTHGTQIGSYFGGELCGVDVDDGTELLLI 480  
DB 421 ASGAPRYQHMGRVLLFQEPQGGGHSQVQTHGTQIGSYFGGELCGVDVDDGTELLLI 480  
QY 481 GAPLFYGEORGRVFIYORROLGFEVSELQDPCGYLGRFGAETALTIDINGGLVDA 540  
DB 481 GAPLFYGEORGRVFIYORROLGFEVSELQDPCGYLGRFGAETALTIDINGGLVDA 540  
QY 541 VGAPLEBQAVYIFNGRHGGLSPQPSQRIEGTOVLSGIQWFGRSIHGVKDEBGLADVA 600  
DB 541 VGAPLEBQAVYIFNGRHGGLSPQPSQRIEGTOVLSGIQWFGRSIHGVKDEBGLADVA 600

QY 601 VGABSONIVLSRPVDMVTLMSPSPAEIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
DB 601 VGABSONIVLSRPVDMVTLMSPSPAEIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
QY 661 POFQGRUVANLTYTLODGHRTTRRGLPFGGRHRLRNIAVTTSMSCDTSFHFVPCVD 720  
DB 661 POFQGRUVANLTYTLODGHRTTRRGLPFGGRHRLRNIAVTTSMSCDTSFHFVPCVD 720  
QY 721 LISPINVSLNFSLWEEBGTPRDQAGKOIPILRPSLSHSTWELPFEKNCGEKCCAN 780  
DB 721 LISPINVSLNFSLWEEBGTPRDQAGKOIPILRPSLSHSTWELPFEKNCGEKCCAN 780  
QY 781 LRVSPSPARSLALTAAPASISVELSLNLEBDAYVQDLHPFGGLSFRKVENLKPBSQ 840  
DB 781 LRVSPSPARSLALTAAPASISVELSLNLEBDAYVQDLHPFGGLSFRKVENLKPBSQ 840  
QY 841 IPVSCBELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSMGDSVELHANVC 900  
DB 841 IPVSCBELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSMGDSVELHANVC 900  
QY 901 NNBDSDLEDNSATTIIPILYPINILIDQEDSTLYSFTPKGPKIHQKMYQVRIQPS 960  
DB 901 NNBDSDLEDNSATTIIPILYPINILIDQEDSTLYSFTPKGPKIHQKMYQVRIQPS 960  
QY 961 IHDNIPITLBAVGVPOPPSEGPITHQWSVQMEPPVPCHEYEDLERLPDAEPCLPGLAFR 1020  
DB 961 IHDNIPITLBAVGVPOPPSEGPITHQWSVQMEPPVPCHEYEDLERLPDAEPCLPGLAFR 1020  
QY 1021 CPVYFROEILVQVGTLELVEGEIETASSMPSLCSSTISFNSSKHHLVGSNASLAQVVMK 1080  
DB 1021 CPVYFROEILVQVGTLELVEGEIETASSMPSLCSSTISFNSSKHHLVGSNASLAQVVMK 1080  
QY 1081 VDVIYKQMLYLYVLSGIGLLILLILFIYLYKVGFFKRNLIKEMKAEAGRGVPNGIPADS 1140  
DB 1081 VDVIYKQMLYLYVLSGIGLLILLILFIYLYKVGFFKRNLIKEMKAEAGRGVPNGIPADS 1140  
QY 1141 EQLASGQAGDPGCLKPLHEKDSBSGGKD 1170  
DB 1141 EQLASGQAGDPGCLKPLHEKDSBSGGKD 1170

RESULT 3  
US-11-080-026-2  
; Sequence 2, Application US/11080026  
; GENERAL INFORMATION:  
; APPLICANT: Springer, Timothy A.  
; APPLICANT: Shimada, Motomu  
; APPLICANT: Liu, Chafen  
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A  
; FILE REFERENCE: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME  
; CURRENT FILING DATE: 2005-03-15  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fastseq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-080-026-2

Query Match 100.0%; Score 6106; DB 7; Length 1170;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDSCITMAMALLSGFFFPASSYNLDVGCARSFSPPRAGRHHGVTLQVGNQVYGA 60  
DB 1 MKDSCITMAMALLSGFFFPASSYNLDVGCARSFSPPRAGRHHGVTLQVGNQVYGA 60

QY 61 PGBGNSTSLYCCSGTGHCLPVTLRGSNTSKYLQMTLADPDDGSLIADCPGSLRCD 120  
DB 61 PGBGNSTSLYCCSGTGHCLPVTLRGSNTSKYLQMTLADPDDGSLIADCPGSLRCD 120  
QY 121 ONTILSGCYLFRONTLOQPMLOGRPGPOECLKGNVDLVFLPDGSMSTLOPDSFOKILDPMK 180  
DB 121 ONTILSGCYLFRONTLOQPMLOGRPGPOECLKGNVDLVFLPDGSMSTLOPDSFOKILDPMK 180  
QY 181 DVMKLSNTSYQFAVOPSTSYKTEFDSYVKKRDPDALIKHYKMLLNTTGAIAVY 240  
DB 181 DVMKLSNTSYQFAVOPSTSYKTEFDSYVKKRDPDALIKHYKMLLNTTGAIAVY 240  
QY 241 ATEVFRBELGARPDATKYLIIITDGEATDSQNDIAAKOIRYIIIGIGHFOTKSSQETLH 300  
DB 241 ATEVFRBELGARPDATKYLIIITDGEATDSQNDIAAKOIRYIIIGIGHFOTKSSQETLH 300  
QY 301 KPAKSPASEFYKIIDTEBKLDLFTLEOKKIYVLEGSTKODLTSFNNELSSSGISADLSR 360  
DB 301 KPAKSPASEFYKIIDTEBKLDLFTLEOKKIYVLEGSTKODLTSFNNELSSSGISADLSR 360  
QY 361 GHAVGAVGANDWAGFIDLKADLQDDTFIGNEBLTPREVAGYLYTWTMPSRQKTSLL 420  
DB 361 GHAVGAVGANDWAGFIDLKADLQDDTFIGNEBLTPREVAGYLYTWTMPSRQKTSLL 420  
QY 421 ASGAPRYQHMGRVILLPOEPQGGHMSQVQTHGTQIGSYFGSELGVVDVDDGETELLII 480  
DB 421 ASGAPRYQHMGRVILLPOEPQGGHMSQVQTHGTQIGSYFGSELGVVDVDDGETELLII 480  
QY 481 GAPLFYGRQGRFITYQRQLGFEVSELOGDGYPGRGAEITALTDTINGGLVDVA 540  
DB 481 GAPLFYGRQGRFITYQRQLGFEVSELOGDGYPGRGAEITALTDTINGGLVDVA 540  
QY 541 VGAPLEBQAVYIYNGRHGGLSPQSORIBETQVLSGIQWFGRIKHVKDLEGGLADVA 600  
DB 541 VGAPLEBQAVYIYNGRHGGLSPQSORIBETQVLSGIQWFGRIKHVKDLEGGLADVA 600  
QY 601 VGABSONIVLSRPVDMVTLMSPSPAEIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
DB 601 VGABSONIVLSRPVDMVTLMSPSPAEIPVHEVCSYSTSNKMEGVNITTCFOIKSLY 660  
QY 661 POFQGRUVANLTYTLODGHRTTRRGLPFGGRHRLRNIAVTTSMSCDTSFHFVPCVD 720  
DB 661 POFQGRUVANLTYTLODGHRTTRRGLPFGGRHRLRNIAVTTSMSCDTSFHFVPCVD 720  
QY 721 LISPINVSLNFSLWEEBGTPRDQAGKOIPILRPSLSHSTWELPFEKNCGEKCCAN 780  
DB 721 LISPINVSLNFSLWEEBGTPRDQAGKOIPILRPSLSHSTWELPFEKNCGEKCCAN 780  
QY 781 LRVSPSPARSLALTAAPASISVELSLNLEBDAYVQDLHPFGGLSFRKVENLKPBSQ 840  
DB 781 LRVSPSPARSLALTAAPASISVELSLNLEBDAYVQDLHPFGGLSFRKVENLKPBSQ 840  
QY 841 IPVSCBELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSMGDSVELHANVC 900  
DB 841 IPVSCBELPEBSRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSMGDSVELHANVC 900  
QY 901 NNBDSDLEDNSATTIIPILYPINILIDQEDSTLYSFTPKGPKIHQKMYQVRIQPS 960  
DB 901 NNBDSDLEDNSATTIIPILYPINILIDQEDSTLYSFTPKGPKIHQKMYQVRIQPS 960  
QY 961 IHDNIPITLBAVGVPOPPSEGPITHQWSVQMEPPVPCHEYEDLERLPDAEPCLPGLAFR 1020  
DB 961 IHDNIPITLBAVGVPOPPSEGPITHQWSVQMEPPVPCHEYEDLERLPDAEPCLPGLAFR 1020  
QY 1021 CPVYFROEILVQVGTLELVEGEIETASSMPSLCSSTISFNSSKHHLVGSNASLAQVVMK 1080  
DB 1021 CPVYFROEILVQVGTLELVEGEIETASSMPSLCSSTISFNSSKHHLVGSNASLAQVVMK 1080  
QY 1081 VDVIYKQMLYLYVLSGIGLLILLILFIYLYKVGFFKRNLIKEMKAEAGRGVPNGIPADS 1140  
DB 1081 VDVIYKQMLYLYVLSGIGLLILLILFIYLYKVGFFKRNLIKEMKAEAGRGVPNGIPADS 1140

RESULT 4  
US-11-107-028-4  
; Sequence 4, Application US/11107028  
; GENERAL INFORMATION:  
; APPLICANT: CHAN, ANDREW C.  
; APPLICANT: GONG, QIAN  
; APPLICANT: MARTIN, FLAVIUS  
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion  
; FILE REFERENCE: P2112R1  
; CURRENT APPLICATION NUMBER: US/11/107,028  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/563,263  
; PRIOR FILING DATE: 2004-04-16  
; NUMBER OF SEQ ID NOS: 52  
; SEQ ID NO 4  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-107-028-4

Query Match 100.0%; Score 6106; DB 7; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKDSCTTMMAMALLSGFFFPAPASYNLDVRGANSFSPRRGRHFGYRVLQVNGVYIGA 60  
Db 1 MKDSCTTMMAMALLSGFFFPAPASYNLDVRGANSFSPRRGRHFGYRVLQVNGVYIGA 60  
Qy 61 PGEKSTSLTQCOCSTGCHCLPVTLRGSNTSKYLGMTLADPTDGSILACDPGLSRTCD 120  
Db 61 PGEKSTSLTQCOCSTGCHCLPVTLRGSNTSKYLGMTLADPTDGSILACDPGLSRTCD 120  
Qy 121 QNTYLSGLCYLFRONTLQGPMLQGRPGQECIKANVDLFLFDGSMLOPDEFOKILDFMK 180  
Db 121 QNTYLSGLCYLFRONTLQGPMLQGRPGQECIKANVDLFLFDGSMLOPDEFOKILDFMK 180  
Qy 181 DVMKTLSTSYQFAAVOSTSYKTEFPDSYVKKRDPALLKHYKMLLNTTGAINV 240  
Db 181 DVMKTLSTSYQFAAVOSTSYKTEFPDSYVKKRDPALLKHYKMLLNTTGAINV 240  
Qy 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIGHFQTKSOETLH 300  
Db 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIIGIGHFQTKSOETLH 300  
Qy 301 KFAKRPASEFVKILDTPEKLDLFTLEOKKIYVLEGSTKODLTSFMELSSSGISADISR 360  
Db 301 KFAKRPASEFVKILDTPEKLDLFTLEOKKIYVLEGSTKODLTSFMELSSSGISADISR 360  
Qy 361 GHAVVAGVAGADWAGGFLDLKADLODPTFIGNBPLTEPVNAGYAGYTTMLPSRQKTSLL 420  
Db 361 GHAVVAGVAGADWAGGFLDLKADLODPTFIGNBPLTEPVNAGYAGYTTMLPSRQKTSLL 420  
Qy 421 ASGAPRYOHMRVLLFOEPGGGSHMSQVQTHGTQISGPGSELGCVUVDGDETELLI 480  
Db 421 ASGAPRYOHMRVLLFOEPGGGSHMSQVQTHGTQISGPGSELGCVUVDGDETELLI 480  
Qy 481 GAPLFYGEORGARFYIYORRQLGFEVSELQDPOYPLGRFGAETALTALDINGDLVVA 540  
Db 481 GAPLFYGEORGARFYIYORRQLGFEVSELQDPOYPLGRFGAETALTALDINGDLVVA 540  
Qy 541 VGAPLEEGGAVYIINGRHGSLSPQSORIEGTQVLSGIQWFGSRHGVKLEGGDLADVA 600  
Db 541 VGAPLEEGGAVYIINGRHGSLSPQSORIEGTQVLSGIQWFGSRHGVKLEGGDLADVA 600  
Qy 601 VGASQMTIVSSRPVMDVMTLMSFPAIIPVHEVCSYSTSNKKEGNTITTCQIKSLY 660  
Db 601 VGASQMTIVSSRPVMDVMTLMSFPAIIPVHEVCSYSTSNKKEGNTITTCQIKSLY 660

Qy 661 POFQGRLVANILTYTLQDGRTRRRGLFPGGRHELRRNIAVTTSMSCTDSPFHPVCVD 720  
Db 661 POFQGRLVANILTYTLQDGRTRRRGLFPGGRHELRRNIAVTTSMSCTDSPFHPVCVD 720  
Qy 721 LISPINVSINPSLMEEGTFRDQAQCKDIPILRPSLHETWEIIPPEKXCGEKKCEAN 780  
Db 721 LISPINVSINPSLMEEGTFRDQAQCKDIPILRPSLHETWEIIPPEKXCGEKKCEAN 780  
Qy 781 LRVSPARARALRLTAPASLVELSLSNLEBDAYWQDLHPFGSLPFKVEMLKPHSQ 840  
Db 781 LRVSPARARALRLTAPASLVELSLSNLEBDAYWQDLHPFGSLPFKVEMLKPHSQ 840  
Qy 841 IIVSCBELPEBSRLSRLSCNVSPIFKAGSHVALQMFNTLVNSSWGDSEIHLAVTC 900  
Db 841 IIVSCBELPEBSRLSRLSCNVSPIFKAGSHVALQMFNTLVNSSWGDSEIHLAVTC 900  
Qy 901 NNEBSDLLEDSATTTIPILYPTNILLQDDEDTLYVSPFKPKKHOUVHMVQVRQPS 960  
Db 901 NNEBSDLLEDSATTTIPILYPTNILLQDDEDTLYVSPFKPKKHOUVHMVQVRQPS 960  
Qy 961 IHDNIPTEBAVVGVPQPESEGITTHQMSVQMEPPVPCHEDELERLPDAEPCLPGALFR 1020  
Db 961 IHDNIPTEBAVVGVPQPESEGITTHQMSVQMEPPVPCHEDELERLPDAEPCLPGALFR 1020  
Qy 1021 CPVVFROEILVOVIGTLELVEIEBASMSFLCSLSISFNSSKHFLYGSNASTLAQVVMK 1080  
Db 1021 CPVVFROEILVOVIGTLELVEIEBASMSFLCSLSISFNSSKHFLYGSNASTLAQVVMK 1080  
Qy 1081 VDVVYERQMTLYVLSIGILLILLIFLYLYKVPFKRNLKXKMEGRGVNPGIAPEDS 1140  
Db 1081 VDVVYERQMTLYVLSIGILLILLIFLYLYKVPFKRNLKXKMEGRGVNPGIAPEDS 1140  
Qy 1141 EQLASGEAGDPGCLKPLHEKDSBSGGKD 1170  
Db 1141 EQLASGEAGDPGCLKPLHEKDSBSGGKD 1170

RESULT 5  
PCT-US05-02350-653  
; Sequence 653, Application PC/TUS0502350  
; GENERAL INFORMATION:  
; APPLICANT: Ayalon-Soffer, Michal  
; APPLICANT: Levine, Zurit  
; APPLICANT: Sella-Tavor, Osnat  
; APPLICANT: Diber, Alex  
; APPLICANT: Shemesh, Ronen  
; APPLICANT: Toporik, Amir  
; APPLICANT: Rotman, Galit  
; APPLICANT: Nemzer, Sergey  
; APPLICANT: Rosenberg, Avi  
; APPLICANT: Dahary, Dvir  
; APPLICANT: Wool, Asaaf  
; APPLICANT: Cojocaru, Gad S.  
; APPLICANT: Akiva, Pinchas  
; APPLICANT: Pollock, Sarah  
; APPLICANT: Savitsky, Kineret  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
; FILE REFERENCE: 28487  
; CURRENT APPLICATION NUMBER: PCT/US05/02350  
; CURRENT FILING DATE: 2005-02-10  
; NUMBER OF SEQ ID NOS: 1155  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 653  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US05-02350-653  
Query Match 99.9%; Score 6098; DB 1; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVGRASFSPPRAGRHRGVRVLOVNGVIVGA 60  
 DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVGRASFSPPRAGRHRGVRVLOVNGVIVGA 60  
 QY 61 PEGNSSTSLVYCCSGTGHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120  
 DB 61 PEGNSSTSLVYCCSGTGHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDVLPFDGSMSLQPDFQKILDFPMK 180  
 DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDVLPFDGSMSLQPDFQKILDFPMK 180  
 QY 181 DVMKLSTNTSYQFAVQFSTSKTEFSDYVKRDPALLKHVGMILLNTTFALINYV 240  
 DB 181 DVMKLSTNTSYQFAVQFSTSKTEFSDYVKRDPALLKHVGMILLNTTFALINYV 240  
 QY 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIKHFQTKESQETLH 300  
 DB 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIKHFQTKESQETLH 300  
 QY 301 KPASKPASEPVKILDTPEKLDLTELQKIIYIEGTSKODLTSFNMELSSSGISADLSR 360  
 DB 301 KPASKPASEPVKILDTPEKLDLTELQKIIYIEGTSKODLTSFNMELSSSGISADLSR 360  
 QY 361 GHAVVAVGAKDMAGGFLDLKADLQDDPTFIGNEBLTPBEVRAGYLGVTWMLPSRQKISL 420  
 DB 361 GHAVVAVGAKDMAGGFLDLKADLQDDPTFIGNEBLTPBEVRAGYLGVTWMLPSRQKISL 420  
 QY 421 ASGARPYOHMGRVLLFOEPQGGHMSOVQTIHGTOIGSYFGSELGCVVDVDDGETELLII 480  
 DB 421 ASGARPYOHMGRVLLFOEPQGGHMSOVQTIHGTOIGSYFGSELGCVVDVDDGETELLII 480  
 QY 481 GAPLFYGBQGRGVFIYORQOLGFEESVELQDPCGYLGRFGAITALTDINGDLVDVA 540  
 DB 481 GAPLFYGBQGRGVFIYORQOLGFEESVELQDPCGYLGRFGAITALTDINGDLVDVA 540  
 QY 541 VGAPLEEGQAVYIIFNGRHGGLSPQPSORIEGTQVLSGIQWFGRSIHGYKDLBGDLADVA 600  
 DB 541 VGAPLEEGQAVYIIFNGRHGGLSPQPSORIEGTQVLSGIQWFGRSIHGYKDLBGDLADVA 600  
 QY 601 VGASEQMTVLSRPVVDWVTLMSFSPARIPIVHEVCSTSTSNKMEGVNITICFOIKSLY 660  
 DB 601 VGASEQMTVLSRPVVDWVTLMSFSPARIPIVHEVCSTSTSNKMEGVNITICFOIKSLY 660  
 QY 661 PQFQRLVANLTYTLQLDGHRTRRRGLFPGGRHRLRNIAVTTSMCTDPSFHPFVQVD 720  
 DB 661 PQFQRLVANLTYTLQLDGHRTRRRGLFPGGRHRLRNIAVTTSMCTDPSFHPFVQVD 720  
 QY 721 LIIPINVSINSLWEEBGTPRDQAKGODIPILPISLHSTWEIPEEKNGCEKCKEAN 780  
 DB 721 LIIPINVSINSLWEEBGTPRDQAKGODIPILPISLHSTWEIPEEKNGCEKCKEAN 780  
 QY 781 LRVSSPARRALRLTAFAISLVEISLNLSEDAWVOLDLHFPGLSFRKXEMLKPSHQ 840  
 DB 781 LRVSSPARRALRLTAFAISLVEISLNLSEDAWVOLDLHFPGLSFRKXEMLKPSHQ 840  
 QY 841 IPIVSCSELPEBSRLSLRALSQVSSPIFKAGHVALQMMFNTLVSSNGDSVELHANVC 900  
 DB 841 IPIVSCSELPEBSRLSLRALSQVSSPIFKAGHVALQMMFNTLVSSNGDSVELHANVC 900  
 QY 901 NNBSDDLSDNSATTIIPILYPINILIDQEDSTLYVSPFKPKIHQVKMYOVRIPS 960  
 DB 901 NNBSDDLSDNSATTIIPILYPINILIDQEDSTLYVSPFKPKIHQVKMYOVRIPS 960  
 QY 961 IHDHNIPTLEAVVGPQPSBGPITHQMSVOMEPVPCHYEDLELPPAAEPCLGALFR 1020  
 DB 961 IHDHNIPTLEAVVGPQPSBGPITHQMSVOMEPVPCHYEDLELPPAAEPCLGALFR 1020  
 QY 1021 CPVVEROBILVQVITGLBLVGBIEKASMSFSLCSSISIFNSKHFLYGSNLSLAQVVMK 1080  
 DB 1021 CPVVEROBILVQVITGLBLVGBIEKASMSFSLCSSISIFNSKHFLYGSNLSLAQVVMK 1080

QY 1081 DVVYEROMLYLYLSGIGILLILLIFLYLYKVFPEKMLKEMKREAGRVNGI PAEDS 1140  
 DB 1081 DVVYEROMLYLYLSGIGILLILLIFLYLYKVFPEKMLKEMKREAGRVNGI PAEDS 1140  
 QY 1141 EQLASQEGADPGCLKPLHEKDESSEGGKD 1170  
 DB 1141 EQLASQEGADPGCLKPLHEKDESSEGGKD 1170  
 RESULT 6  
 US-09-976-935A-36  
 ; Sequence 36, Application US/0976935A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Staunton, Donald E.  
 ; TITLE OF INVENTION: MATERIALS AND METHODS TO MODULATE LIGAND BINDING/ENZYMATIC ACTIVI  
 ; TITLE OF INVENTION: OF ALPHA/BETA PROTEINS CONTAINING AN ALLOSTERIC REGULATORY SITE  
 ; FILE REFERENCE: 27866/36470A  
 ; CURRENT APPLICATION NUMBER: US/09/976,935A  
 ; CURRENT FILING DATE: 2001-10-12  
 ; PRIOR APPLICATION NUMBER: US 60/239,750  
 ; PRIOR FILING DATE: 2000-10-12  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 36  
 ; LENGTH: 1170  
 ; TYPE: PRT  
 ; ORGANISM: amino acid sequence of LFA-1  
 ; US-09-976-935A-36  
 Query Match 99.9%; Score 6098; DB 5; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVGRASFSPPRAGRHRGVRVLOVNGVIVGA 60  
 DB 1 MKDSCITVMAMALLSGFFFPAPASSYNLDVGRASFSPPRAGRHRGVRVLOVNGVIVGA 60  
 QY 61 PEGNSSTSLVYCCSGTGHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120  
 DB 61 PEGNSSTSLVYCCSGTGHCLPVTLRGNSNTSKYLGMTLATDPTDGSILACDPGLSRTCD 120  
 QY 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDVLPFDGSMSLQPDFQKILDFPMK 180  
 DB 121 QNTYLSGLCYLFRONLQGPMLQGRPGFQECIKGNVDVLPFDGSMSLQPDFQKILDFPMK 180  
 QY 181 DVMKLSTNTSYQFAVQFSTSKTEFSDYVKRDPALLKHVGMILLNTTFALINYV 240  
 DB 181 DVMKLSTNTSYQFAVQFSTSKTEFSDYVKRDPALLKHVGMILLNTTFALINYV 240  
 QY 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIKHFQTKESQETLH 300  
 DB 241 ATEVREBELGARPDATKVLIIITDGEATDSGNIDAADIIIRYIIGIKHFQTKESQETLH 300  
 QY 301 KPASKPASEPVKILDTPEKLDLTELQKIIYIEGTSKODLTSFNMELSSSGISADLSR 360  
 DB 301 KPASKPASEPVKILDTPEKLDLTELQKIIYIEGTSKODLTSFNMELSSSGISADLSR 360  
 QY 361 GHAVVAVGAKDMAGGFLDLKADLQDDPTFIGNEBLTPBEVRAGYLGVTWMLPSRQKISL 420  
 DB 361 GHAVVAVGAKDMAGGFLDLKADLQDDPTFIGNEBLTPBEVRAGYLGVTWMLPSRQKISL 420  
 QY 421 ASGARPYOHMGRVLLFOEPQGGHMSOVQTIHGTOIGSYFGSELGCVVDVDDGETELLII 480  
 DB 421 ASGARPYOHMGRVLLFOEPQGGHMSOVQTIHGTOIGSYFGSELGCVVDVDDGETELLII 480  
 QY 481 GAPLFYGBQGRGVFIYORQOLGFEESVELQDPCGYLGRFGAITALTDINGDLVDVA 540  
 DB 481 GAPLFYGBQGRGVFIYORQOLGFEESVELQDPCGYLGRFGAITALTDINGDLVDVA 540  
 QY 541 VGAPLEEGQAVYIIFNGRHGGLSPQPSORIEGTQVLSGIQWFGRSIHGYKDLBGDLADVA 600  
 DB 541 VGAPLEEGQAVYIIFNGRHGGLSPQPSORIEGTQVLSGIQWFGRSIHGYKDLBGDLADVA 600

Qy 601 VGASQMIIVLSRPVDMVTLMSPSPAEI PVHVEVCSYSTSNKMGVNTTICFOIKSLY 660  
Db 601 VGASQMIIVLSRPVDMVTLMSPSPAEI PVHVEVCSYSTSNKMGVNTTICFOIKSLY 660  
Qy 661 POFQGRIVANITTYTLQDGHRTTRRGLFPGGRIELRRNIATVTTSMCTDPSFHPVCYQD 720  
Db 661 POFQGRIVANITTYTLQDGHRTTRRGLFPGGRIELRRNIATVTTSMCTDPSFHPVCYQD 720  
Qy 721 LISPIVNSLNFSLMBEETPRDQAOQKDIPIILRPSLHSETWEIPEKNGGDKKCEAN 780  
Db 721 LISPIVNSLNFSLMBEETPRDQAOQKDIPIILRPSLHSETWEIPEKNGGDKKCEAN 780  
Qy 781 LRVSPSPARARLRTAFASLSVELSLSNLEBDAYWQDLHPPGSLSPKRVEMLKPHSQ 840  
Db 781 LRVSPSPARARLRTAFASLSVELSLSNLEBDAYWQDLHPPGSLSPKRVEMLKPHSQ 840  
Qy 841 IPVSCBELPEESRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSSWGDSEVELHANVTC 900  
Db 841 IPVSCBELPEESRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSSWGDSEVELHANVTC 900  
Qy 901 NNEBSDLLEDSATTTIPIILYPINILIQDQEDSTLYVSFTPKGPKIHQVKHMYQVRIQPS 960  
Db 901 NNEBSDLLEDSATTTIPIILYPINILIQDQEDSTLYVSFTPKGPKIHQVKHMYQVRIQPS 960  
Qy 961 IHDNIPITLBAVGVQPPSESGPITTHQWSVQMEPPVPCHYEDLERLPDAEPCLPGALFR 1020  
Db 961 IHDNIPITLBAVGVQPPSESGPITTHQWSVQMEPPVPCHYEDLERLPDAEPCLPGALFR 1020  
Qy 1021 CPVYFRQGIIVQVIGTLELVGEIRASWFSICSSISISFNSSKIFHLVGSNASTLAQVYMK 1080  
Db 1021 CPVYFRQGIIVQVIGTLELVGEIRASWFSICSSISISFNSSKIFHLVGSNASTLAQVYMK 1080  
Qy 1081 VDVIYKEMKLYLYLSGIGLLLLFIYLVKYVGFGRNLKEKMEAGRGVPGNIGLPADS 1140  
Db 1081 VDVIYKEMKLYLYLSGIGLLLLFIYLVKYVGFGRNLKEKMEAGRGVPGNIGLPADS 1140  
Qy 1141 EQLASQGEAGDPGCLKPLHEKDSBSGGKD 1170  
Db 1141 EQLASQGEAGDPGCLKPLHEKDSBSGGKD 1170

RESULT 7  
US-11-043-770-653  
; Sequence 653, Application US/11043770  
; GENERAL INFORMATION:  
; APPLICANT: Avalon-Soffer, Michal  
; APPLICANT: Levine, Zurit  
; APPLICANT: Sella-Tavor, Osnat  
; APPLICANT: Diber, Alex  
; APPLICANT: Shemesh, Ronen  
; APPLICANT: Toporik, Amir  
; APPLICANT: Rotman, Galit  
; APPLICANT: Nemzer, Sergey  
; APPLICANT: Rosenberg, Avi  
; APPLICANT: Wool, Asaaf  
; APPLICANT: Cojocaru, Gad S.  
; APPLICANT: Aliva, Pinchas  
; APPLICANT: Pollock, Sarah  
; APPLICANT: Savitsky, Jeanette  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING  
; FILE REFERENCE: 26488  
; CURRENT APPLICATION NUMBER: US/11/043,770  
; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 1155  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 653  
; LENGTH: 1170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-043-770-653

Query Match 99.9%; Score 6098; DB 7; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKDSCITVAMALLSGFFPPAPASSYNLDVGRARSPPRPAHFGYRVLQVANGVIVA 60  
Db 1 MKDSCITVAMALLSGFFPPAPASSYNLDVGRARSPPRPAHFGYRVLQVANGVIVA 60  
Qy 61 PGEAGNSTGSLYQOOSGTHCLPTVLRGNSNTSKYLQMTLATDPTDGSIIACDGLSRTCD 120  
Db 61 PGEAGNSTGSLYQOOSGTHCLPTVLRGNSNTSKYLQMTLATDPTDGSIIACDGLSRTCD 120  
Qy 121 QNTYLSGLCYLFRONLOGPMLQGRPGQECIKGNVDVLFPLDSMSLOPDEFOKILDFPMK 180  
Db 121 QNTYLSGLCYLFRONLOGPMLQGRPGQECIKGNVDVLFPLDSMSLOPDEFOKILDFPMK 180  
Qy 181 DVMKKLSNTSYQFAAVQFSTSYKTEPFDSDYVRKDPDALLKHKVKNMLLTNTFGAIVNY 240  
Db 181 DVMKKLSNTSYQFAAVQFSTSYKTEPFDSDYVRKDPDALLKHKVKNMLLTNTFGAIVNY 240  
Qy 241 ATEVFREELGARPDATVLIITDGEATDSGNIDAAKDIIRYIIGIKHQTQTESQETLH 300  
Db 241 ATEVFREELGARPDATVLIITDGEATDSGNIDAAKDIIRYIIGIKHQTQTESQETLH 300  
Qy 301 KFASKPASEFVKIIDPFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSSGISADLSR 360  
Db 301 KFASKPASEFVKIIDPFEKLDLFTLEOKKIYIEGTSKODLTSFNMELSSSGISADLSR 360  
Qy 361 GHAVAVGAKDAGGFLDKADLQDDTFIGNEPLTPEVAVAGLYGTVTMLPSRQKTSLL 420  
Db 361 GHAVAVGAKDAGGFLDKADLQDDTFIGNEPLTPEVAVAGLYGTVTMLPSRQKTSLL 420  
Qy 421 ASGAPRYQHMGKRVLLPOEPGGHMSOVQTHQTOIGSYVGGELCGVDVQDDETELLI 480  
Db 421 ASGAPRYQHMGKRVLLPOEPGGHMSOVQTHQTOIGSYVGGELCGVDVQDDETELLI 480  
Qy 481 GAPLFYGEORQGVFIYQRRQLGFESEVSELQDPGYLAFRGEATITATDINDGLADVA 540  
Db 481 GAPLFYGEORQGVFIYQRRQLGFESEVSELQDPGYLAFRGEATITATDINDGLADVA 540  
Qy 541 VGAPLEBQGAUYIIFNGRHGSLSPQPSORIIGTOVLSGIOMFGRSIHGVKDLBBDGLADVA 600  
Db 541 VGAPLEBQGAUYIIFNGRHGSLSPQPSORIIGTOVLSGIOMFGRSIHGVKDLBBDGLADVA 600  
Qy 601 VGASQMIIVLSRPVDMVTLMSPSPAEI PVHVEVCSYSTSNKMGVNTTICFOIKSLY 660  
Db 601 VGASQMIIVLSRPVDMVTLMSPSPAEI PVHVEVCSYSTSNKMGVNTTICFOIKSLY 660  
Qy 661 POFQGRIVANITTYTLQDGHRTTRRGLFPGGRIELRRNIATVTTSMCTDPSFHPVCYQD 720  
Db 661 POFQGRIVANITTYTLQDGHRTTRRGLFPGGRIELRRNIATVTTSMCTDPSFHPVCYQD 720  
Qy 721 LISPIVNSLNFSLMBEETPRDQAOQKDIPIILRPSLHSETWEIPEKNGGDKKCEAN 780  
Db 721 LISPIVNSLNFSLMBEETPRDQAOQKDIPIILRPSLHSETWEIPEKNGGDKKCEAN 780  
Qy 781 LRVSPSPARARLRTAFASLSVELSLSNLEBDAYWQDLHPPGSLSPKRVEMLKPHSQ 840  
Db 781 LRVSPSPARARLRTAFASLSVELSLSNLEBDAYWQDLHPPGSLSPKRVEMLKPHSQ 840  
Qy 841 IPVSCBELPEESRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSSWGDSEVELHANVTC 900  
Db 841 IPVSCBELPEESRLSRALSCNVSSPIFKAGHSVALQMMFNTLVNSSWGDSEVELHANVTC 900  
Qy 901 NNEBSDLLEDSATTTIPIILYPINILIQDQEDSTLYVSFTPKGPKIHQVKHMYQVRIQPS 960  
Db 901 NNEBSDLLEDSATTTIPIILYPINILIQDQEDSTLYVSFTPKGPKIHQVKHMYQVRIQPS 960  
Qy 961 IHDNIPITLBAVGVQPPSESGPITTHQWSVQMEPPVPCHYEDLERLPDAEPCLPGALFR 1020  
Db 961 IHDNIPITLBAVGVQPPSESGPITTHQWSVQMEPPVPCHYEDLERLPDAEPCLPGALFR 1020

QY 1021 CPVFRQELIVQVIGTLELVEIBASSNFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
DB 1021 CPVFRQELIVQVIGTLELVEIBASSNFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
QY 1081 VDVIYKQMLYLYLSGIGLLLLLFIVLYKVGFFKRNKKEKMEAGRGVNGI PAEDS 1140  
DB 1081 VDVIYKQMLYLYLSGIGLLLLLFIVLYKVGFFKRNKKEKMEAGRGVNGI PAEDS 1140  
QY 1141 EQLASQGEADPGCLKPLHKDSESGGKD 1170  
DB 1141 EQLASQGEADPGCLKPLHKDSESGGKD 1170

## RESULT 8

US-11-062-290-1  
Sequence 1, Application US/11062290  
GENERAL INFORMATION:  
APPLICANT: KAPUSTAY, PAMELA M.  
APPLICANT: LEWIS, REX H.  
TITLE OF INVENTION: LFA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE  
FILE REFERENCE: 046007/0272304  
CURRENT APPLICATION NUMBER: US/11/062,290  
CURRENT FILING DATE: 2005-02-17  
PRIOR APPLICATION NUMBER: US/10/261,164  
PRIOR FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1170  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-062-290-1

Query Match 99.9%; Score 6098; DB 7; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDSCITTMAMALLSGFFFPASSYNLDVKGASFPSPRAGRHFGRVLOVNGVYGA 60  
DB 1 MKDSCITTMAMALLSGFFFPASSYNLDVKGASFPSPRAGRHFGRVLOVNGVYGA 60  
QY 61 PGBNSTSLYQCCSGTGHCLPVTLLRGSNTSKYLGMTLADPTDGSILACDPGLSRCD 120  
DB 61 PGBNSTSLYQCCSGTGHCLPVTLLRGSNTSKYLGMTLADPTDGSILACDPGLSRCD 120  
QY 121 QNTYLSGLCYLFRONTLQSPMLQGRPGQECIKGNVDLFLFDGSMSLQPDFOKILDPMK 180  
DB 121 QNTYLSGLCYLFRONTLQSPMLQGRPGQECIKGNVDLFLFDGSMSLQPDFOKILDPMK 180  
QY 181 DVNKKLSTSYQFAAVQSTSYKTEPDSYVKRDPDALLKHYKMLLTNTFGAINV 240  
DB 181 DVNKKLSTSYQFAAVQSTSYKTEPDSYVKRDPDALLKHYKMLLTNTFGAINV 240  
QY 241 ATYVREBELGARPRATKYLIIITDGEATDSGNIDAADIIYIIGIGHFQTKESQETLH 300  
DB 241 ATYVREBELGARPRATKYLIIITDGEATDSGNIDAADIIYIIGIGHFQTKESQETLH 300  
QY 301 KFAKSPASEFYKIDTFEKLKDLFTELQKIIYIEGTSKODLTSFNNMELSSGSIADLSR 360  
DB 301 KFAKSPASEFYKIDTFEKLKDLFTELQKIIYIEGTSKODLTSFNNMELSSGSIADLSR 360  
QY 361 GHAVVGAAGADWAGFLDLKADLDDTFIGNEPILTEPVARAGYLGTYVWLPSRQKTSLL 420  
DB 361 GHAVVGAAGADWAGFLDLKADLDDTFIGNEPILTEPVARAGYLGTYVWLPSRQKTSLL 420  
QY 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVQTHGTQIGYFGBELCGVVDVDDGETELLII 480  
DB 421 ASGAPRYQHMGRVLLFQEPQGGHMSQVQTHGTQIGYFGBELCGVVDVDDGETELLII 480  
QY 481 GAPLFYGBORGGRVFIYQRRQLGFEVEVSELQDDEPPLGRGEGAITALTIDINGGLVDVA 540  
DB 481 GAPLFYGBORGGRVFIYQRRQLGFEVEVSELQDDEPPLGRGEGAITALTIDINGGLVDVA 540

QY 541 VGAPLEBOGAVYIFNGHGGSLPQSPQRIGCTOVLSCIQMGFRSHGVKDLBEGDLADVA 600  
DB 541 VGAPLEBOGAVYIFNGHGGSLPQSPQRIGCTOVLSCIQMGFRSHGVKDLBEGDLADVA 600  
QY 601 VGASQMTIVLSSRPVDMVTLMSRPAEIPVHEVECSYTSNKKRSGVNTTICFOIKSLY 660  
DB 601 VGASQMTIVLSSRPVDMVTLMSRPAEIPVHEVECSYTSNKKRSGVNTTICFOIKSLY 660  
QY 661 PQQGRVLANVLTLOLDGHRTRRGLPGRRHRLRNIAVTTSMSTCDSEFHPVQVD 720  
DB 661 PQQGRVLANVLTLOLDGHRTRRGLPGRRHRLRNIAVTTSMSTCDSEFHPVQVD 720  
QY 721 LISPIVSLNFSLWEEGTPRDQAOQKDIPILRPSLSETEWIEPERKCGEDKCEAN 780  
DB 721 LISPIVSLNFSLWEEGTPRDQAOQKDIPILRPSLSETEWIEPERKCGEDKCEAN 780  
QY 781 LRVSFSPARARALRTAFASLVELSISNLEDAVYVOLDLHPPGSLFRKVEMLKPSQ 840  
DB 781 LRVSFSPARARALRTAFASLVELSISNLEDAVYVOLDLHPPGSLFRKVEMLKPSQ 840  
QY 841 IPVSCBELPERSRLSRALSQVSSPIFKAGHSVALQMMNTLVNSSWGSVELHANVTC 900  
DB 841 IPVSCBELPERSRLSRALSQVSSPIFKAGHSVALQMMNTLVNSSWGSVELHANVTC 900  
QY 901 NNEDSDLEONSATTTIPILPINILQDOEDSTLYVSPKPKIHQVKNTOVRLOPS 960  
DB 901 NNEDSDLEONSATTTIPILPINILQDOEDSTLYVSPKPKIHQVKNTOVRLOPS 960  
QY 961 IHDNIPTEAAVGVPPQSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGLAFR 1020  
DB 961 IHDNIPTEAAVGVPPQSEGPITTHQMSVQMEPPVCHYEDLERLPDAEPCLPGLAFR 1020  
QY 1021 CPVFRQELIVQVIGTLELVEIBASSNFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
DB 1021 CPVFRQELIVQVIGTLELVEIBASSNFSLCSLSISFNSSKHFHLYGSNASTLAQVVMK 1080  
QY 1081 VDVIYKQMLYLYLSGIGLLLLLFIVLYKVGFFKRNKKEKMEAGRGVNGI PAEDS 1140  
DB 1081 VDVIYKQMLYLYLSGIGLLLLLFIVLYKVGFFKRNKKEKMEAGRGVNGI PAEDS 1140  
QY 1141 EQLASQGEADPGCLKPLHKDSESGGKD 1170  
DB 1141 EQLASQGEADPGCLKPLHKDSESGGKD 1170

## RESULT 9

PCT-US03-10870-295  
Sequence 295, Application PC/TUS0310870  
GENERAL INFORMATION:  
APPLICANT: Mitokor, Inc.  
APPLICANT: Buck Institute  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Fahy, Eoin D.  
APPLICANT: Zhang, Bing  
APPLICANT: Gibson, Bradford W.  
APPLICANT: Taylor, Steven W.  
APPLICANT: Glenn, Gary M.  
APPLICANT: Marnock, Dale B.  
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
FILE REFERENCE: 660088.465PC  
CURRENT APPLICATION NUMBER: PCT/US03/10870  
CURRENT FILING DATE: 2003-04-04  
NUMBER OF SEQ ID NOS: 3025  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 295  
LENGTH: 1223  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US03-10870-295

Query Match 99.1%; Score 6053.5; DB 1; Length 1223;  
Best Local Similarity 95.5%; Pred. No. 0;

Matches 1168; Conservative 0; Mismatches 2; Indels 53; Gaps 1;

```

Qy 1 MKDSGITMAMALLSGFFFPAPASSYNLDVGAFFSPRAGRHRGVYLVQNGVYGA 60
Db 1 MKDSGITMAMALLSGFFFPAPASSYNLDVGAFFSPRAGRHRGVYLVQNGVYGA 60
Qy 61 PGBNGSTSLYQCSGTHCLPVTLRGNSYTSKYLGMTATDPTDGSILACDPGLSRTCD 120
Db 61 PGBNGSTSLYQCSGTHCLPVTLRGNSYTSKYLGMTATDPTDGSILACDPGLSRTCD 120
Qy 121 QNTYLSGICLYFRONTLOQPMLOGRPGFOECIKGNVDVLPFLDGSMSLOPDEFOKILDPMK 180
Db 121 QNTYLSGICLYFRONTLOQPMLOGRPGFOECIKGNVDVLPFLDGSMSLOPDEFOKILDPMK 180
Qy 181 DVMKCLSTSYOPAVOFSYKTEFDFSDVYKRRDPAALLKHVKNMILLNTGAINVY 240
Db 181 DVMKCLSTSYOPAVOFSYKTEFDFSDVYKRRDPAALLKHVKNMILLNTGAINVY 240
Qy 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIGIGHFQTKESQETLH 300
Db 241 ATEVFRBELGARPDATKVLIIITDGEATDSGNIDAADKIIRYIIGIGHFQTKESQETLH 300
Qy 301 KFAKSPASEFYKIIDTFPEKLDLPTELQKIVIEGTSKODLTSENMELSSSGISADISR 360
Db 301 KFAKSPASEFYKIIDTFPEKLDLPTELQKIVIEGTSKODLTSENMELSSSGISADISR 360
Qy 361 GHAVVGAAGAKMAGGFLDLKADLODDPFIENEPLEPRVARGYLYTWTMLPSRQKSTLL 420
Db 361 GHAVVGAAGAKMAGGFLDLKADLODDPFIENEPLEPRVARGYLYTWTMLPSRQKSTLL 420
Qy 421 ASGARPYOMGRVLLFOEPQGGHMSQVOTIHGTQIGSYFGSELGVVDODGETELLII 480
Db 421 ASGARPYOMGRVLLFOEPQGGHMSQVOTIHGTQIGSYFGSELGVVDODGETELLII 480
Qy 481 GARPFLYEGORGRVFIYORROLGFEVESELQGDPEYPLGRFGEAITALTINDGCLVDA 540
Db 481 GARPFLYEGORGRVFIYORROLGFEVESELQGDPEYPLGRFGEAITALTINDGCLVDA 540
Qy 541 VGAPLEBEGAVYINFRHGGSLPOPSQIEGTQVLSGIQWGRSRHGVKLEGGGLADVA 600
Db 541 VGAPLEBEGAVYINFRHGGSLPOPSQIEGTQVLSGIQWGRSRHGVKLEGGGLADVA 600
Qy 601 VGASOMIVLSSRPVDMVTLMSPSPAIPIVHEVECSYSTSNKMEGVNITICQIKSLY 660
Db 601 VGASOMIVLSSRPVDMVTLMSPSPAIPIVHEVECSYSTSNKMEGVNITICQIKSLY 660
Qy 661 POFQGRIVANTTYTLQDGHRTRRRGLPGRGHEIRRNIAVTTSMSCDPSFHPVCYQD 720
Db 661 POFQGRIVANTTYTLQDGHRTRRRGLPGRGHEIRRNIAVTTSMSCDPSFHPVCYQD 720
Qy 721 LISPIVNSLNSLMBEESTPRDORAQKDIPILRPSLSHSTWRIPEKNGGDEKCGAN 780
Db 721 LISPIVNSLNSLMBEESTPRDORAQKDIPILRPSLSHSTWRIPEKNGGDEKCGAN 780
Qy 781 LRVFSFSPARSALNLTAFASLSVELSLNLEDAVWOLDLHFPFGSLFRKYEMLKPHSQ 840
Db 781 LRVFSFSPARSALNLTAFASLSVELSLNLEDAVWOLDLHFPFGSLFRKYEMLKPHSQ 840
Qy 841 IPVSCBELPEBSRLISRALSCNVSSPIFKAGHSVALQMMFNTLVNMSGDSVELHANVC 900
Db 841 IPVSCBELPEBSRLISRALSCNVSSPIFKAGHSVALQMMFNTLVNMSGDSVELHANVC 900
Qy 901 NNEGSDILLENSATTIPIILYPINILLQDQSDSTLYVFTPKGPIHVKMYOGVHGLV 960
Db 901 NNEGSDILLENSATTIPIILYPINILLQDQSDSTLYVFTPKGPIHVKMYOGVHGLV 960
Qy 955 -----VRIQPSIHDHNP 967
Db 955 -----VRIQPSIHDHNP 967
Qy 961 EMQTSKOTLCRPAGDAEHTVGAQGEGLPCPWGVBSAPFNDNIRAGCRRIQPSIHDHNP 1020
Db 961 EMQTSKOTLCRPAGDAEHTVGAQGEGLPCPWGVBSAPFNDNIRAGCRRIQPSIHDHNP 1020
Qy 968 TLEAVGVGPPDSGPIITHQMSVQMEPPVPCHYEDLERLPDAABECLFGALFRGVVFRQ 1027
Db 968 TLEAVGVGPPDSGPIITHQMSVQMEPPVPCHYEDLERLPDAABECLFGALFRGVVFRQ 1027
Qy 1021 TLEAVGVGPPDSGPIITHQMSVQMEPPVPCHYEDLERLPDAABECLFGALFRGVVFRQ 1080
Db 1021 TLEAVGVGPPDSGPIITHQMSVQMEPPVPCHYEDLERLPDAABECLFGALFRGVVFRQ 1080

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Qy 1028 EILVQVITGLTELYGEIRASSMPSLCSLSISFNSSKHFLHYGSNASLAQVVMKVDDVYER 1087
Db 1081 EILVQVITGLTELYGEIRASSMPSLCSLSISFNSSKHFLHYGSNASLAQVVMKVDDVYER 1140
Qy 1088 QMLTYVLSGIGILLLLLLFIYLYKVGPFKRNKEMEAARGVPNGIPADESEQLASGQ 1147
Db 1141 QMLTYVLSGIGILLLLLLFIYLYKVGPFKRNKEMEAARGVPNGIPADESEQLASGQ 1200
Qy 1148 EAGDPGLKPLHEKDSRSGGKD 1170
Db 1201 EAGDPGLKPLHEKDSRSGGKD 1223

RESULT 10
US-11-021-951-130
; Sequence 130, Application US/11021951
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHREIDIG, Andreas
; APPLICANT: VOTSMER, Christian
; APPLICANT: Ketting, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.000205
; CURRENT APPLICATION NUMBER: US/11/021.951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/072.198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543.518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524.960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-130

Query Match 98.0%; Score 5981; DB 7; Length 1145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      241 EATSDGNDAADIIIRYIIIGIKHQTKEOETLHKFASKPAKSEVVKILDTREKLDLPT 300
Qy      336 ELQKKIYIIEGTSKODLTSFNNELSSSGISADLSRGHVAVGAKDVAAGFLDKADLQ 385
Db      301 ELQKKIYIIEGTSKODLTSFNNELSSSGISADLSRGHVAVGAKDVAAGFLDKADLQ 360
Qy      366 DDTFIGNELTPEVPAQYIGYVTVMLPSRQKTSLLASGAPRYQHMGRVLLFQEPQGGHW 445
Db      361 DDTFIGNELTPEVPAQYIGYVTVMLPSRQKTSLLASGAPRYQHMGRVLLFQEPQGGHW 420
Qy      446 SOVOTIHGQISYSGELCGVDVDDGETELLIGAPFYEGORGRFITYOROLPE 505
Db      421 SOVOTIHGQISYSGELCGVDVDDGETELLIGAPFYEGORGRFITYOROLPE 480
Qy      506 EVSELOQDPGYPLGFGEALITALTINDGLVDVAVGAFLBEGQAVYIFNGHGLSP 565
Db      481 EVSELOQDPGYPLGFGEALITALTINDGLVDVAVGAFLBEGQAVYIFNGHGLSP 540
Qy      566 SQRIEGTQVLSGIQWFGRSIHGVKDLBEGDLADVAVGAESQMIVLSRPVDMVTLMSPS 625
Db      541 SQRIEGTQVLSGIQWFGRSIHGVKDLBEGDLADVAVGAESQMIVLSRPVDMVTLMSPS 600
Qy      636 PABIVHVEECYSYTSNNKKEGVNITICFOIKSLYPOFGRLVANULTYLLQDGHRTRR 685
Db      601 PABIVHVEECYSYTSNNKKEGVNITICFOIKSLYPOFGRLVANULTYLLQDGHRTRR 660
Qy      666 GLPFGGRHRLRNIAVTTSMSCDPSFHPVPCVODLISPINVSINPSLMBEERTPRDRA 745
Db      661 GLPFGGRHRLRNIAVTTSMSCDPSFHPVPCVODLISPINVSINPSLMBEERTPRDRA 720
Qy      746 QGKDIPIILRPSLSHETWEIPEKNCGEDKCEANLRSFSPARSALRLTAPASLVEL 805
Db      721 QGKDIPIILRPSLSHETWEIPEKNCGEDKCEANLRSFSPARSALRLTAPASLVEL 780
Qy      806 SLGSLNEEDAYVQDLHFPFGSLSPKVEMLKPHSQIPVSCBELPEESRLLSALSCNVSS 865
Db      781 SLGSLNEEDAYVQDLHFPFGSLSPKVEMLKPHSQIPVSCBELPEESRLLSALSCNVSS 840
Qy      866 PLFKAGHVALQOMENTLVNSSWGDSVBLHANVTGNEDSDLEENSAITIIPIIYPINI 925
Db      841 PLFKAGHVALQOMENTLVNSSWGDSVBLHANVTGNEDSDLEENSAITIIPIIYPINI 900
Qy      926 LIQDDESDTLVYSFTPKGPKIHQVGMQVRIQPSIHDHNIPTLEAVVGVPOPSSEGIT 985
Db      901 LIQDDESDTLVYSFTPKGPKIHQVGMQVRIQPSIHDHNIPTLEAVVGVPOPSSEGIT 960
Qy      986 HQMSVQMBEPVPCYHEDLERLPDAAPCLPGALFRCPVFRQELIVOVIGTLELVEIEA 1045
Db      961 HQMSVQMBEPVPCYHEDLERLPDAAPCLPGALFRCPVFRQELIVOVIGTLELVEIEA 1020
Qy      1046 SSMFSLCSLSLISFNSSSKHFLYGSNASLAQVVMKVYVYERKOMLYLVLSGIGELLLL 1105
Db      1021 SSMFSLCSLSLISFNSSSKHFLYGSNASLAQVVMKVYVYERKOMLYLVLSGIGELLLL 1080
Qy      1106 LIFFILVYKGFPRKULKEKMBAGRVNNGIIPADESEOLASGEADPGCLRHKHSDS 1165
Db      1081 LIFFILVYKGFPRKULKEKMBAGRVNNGIIPADESEOLASGEADPGCLRHKHSDS 1140
Qy      1166 GGGKD 1170
Db      1141 GGGKD 1145

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```

; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONRIAL PROTEOME
; FILE REFERENCE: 660088.465PC
; CURRENT APPLICATION NUMBER: PCT/US03/10870
; NUMBER OF SEQ ID NOS: 2003-04-04
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1871
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10870-1871

Query Match      91.5%; Score 5585; DB 1; Length 1086;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1085; Conservative 0; Mismatches 1; Indels 84; Gaps 2;

Qy      1 MKDSCTVMAMALISGFFFPAPASSYNDVARGASFPSPRGRHFGYRVLOVNGVYIGA 60
Db      1 MKDSCTVMAMALISGFFFPAPASSYNDVARGASFPSPRGRHFGYRVLOVNGVYIGA 60
Qy      61 PEGNSTGSLYQCSGTGHCPLVTLRGSNTSKYLGMTLATDPDGSILACDPLSRYCD 120
Db      61 PEGNSTGSLYQCSGTGHCPLVTLRGSNTSKYLGMTLATDPDGSILACDPLSRYCD 109
Qy      121 QNTYLSGLCYLFRONLQGPMLQGRPGQECIKGNVDLVFLFDGSMISLOPDEFQKIDPMK 180
Db      110 ----- 109
Qy      181 DVMKSLNYSQFAAVQESTSYKTEFDESDVYKRDPAALKHYKHMILLTNTGALINY 240
Db      110 -----FAAVQESTSYKTEFDESDVYKRDPAALKHYKHMILLTNTGALINY 157
Qy      241 ATEVREELGARPDATKYLIIITGAEATDSGNDAADIIIRYIIIGIKHQTKEOETLH 300
Db      158 ATEVREELGARPDATKYLIIITGAEATDSGNDAADIIIRYIIIGIKHQTKEOETLH 217
Qy      301 KFAKSPABEPYKIIDTEKLDLFTLEOKKIYIIEGTSKODLTSFNNELSSSGISADLSR 360
Db      218 KFAKSPABEPYKIIDTEKLDLFTLEOKKIYIIEGTSKODLTSFNNELSSSGISADLSR 277
Qy      361 GHAVVGAAGADWAGGFLDLKADLQDPTFIGNEBLTPVPAQYIGYVTVMLPSRQKTSLL 420
Db      278 GHAVVGAAGADWAGGFLDLKADLQDPTFIGNEBLTPVPAQYIGYVTVMLPSRQKTSLL 337
Qy      421 ASGA.PRYOHMGRVLLFQEPQGGHMSOVQTIHGQISYFGGELCGVDVDDGETELLII 480
Db      338 ASGA.PRYOHMGRVLLFQEPQGGHMSOVQTIHGQISYFGGELCGVDVDDGETELLII 397
Qy      481 GAPLFYGBORGRFITYOROLGFEVSELOQDPGYPLGFGEALITALTINDGLVDVA 540
Db      398 GAPLFYGBORGRFITYOROLGFEVSELOQDPGYPLGFGEALITALTINDGLVDVA 457
Qy      541 VGAPLEBQAVYIFNGHGLSPQSORIESTQVLSGIQWFGRSIHGVKDLBEGDLADVA 600
Db      458 VGAPLEBQAVYIFNGHGLSPQSORIESTQVLSGIQWFGRSIHGVKDLBEGDLADVA 517
Qy      601 VGASQMIVLSRPVDMVTLMSPSPAIIPHVEECYSYTSNNKKEGVNITICFOIKSLY 660
Db      518 VGASQMIVLSRPVDMVTLMSPSPAIIPHVEECYSYTSNNKKEGVNITICFOIKSLY 577
Qy      661 POFQGRIVANULTYLLQDGHRTRRGLFPGGRHRLRNIAVTTSMSCDPSFHPVPCVOD 720
Db      578 POFQGRIVANULTYLLQDGHRTRRGLFPGGRHRLRNIAVTTSMSCDPSFHPVPCVOD 637
Qy      721 LISPINVSINPSLMBEERTPRDRAQKDIPIILRPSLSHETWEIPEKNCGEDKCEAN 780
Db      638 LISPINVSINPSLMBEERTPRDRA-GKDIPIILRPSLSHETWEIPEKNCGEDKCEAN 696
Qy      781 LRVSFSPARSALRLTAPASLVELSLGNEEDAYVWQDLHFPFGSLSPKVEMLKPHSQ 840

```

RESULT 11  
PCT-US03-10870-1871  
Sequence 1871, Application PC/TUS0310870  
GENERAL INFORMATION:

APPLICANT: Mitokor, Inc.  
APPLICANT: Buck Institute  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Fahy, Bojin D.  
APPLICANT: Zhang, Bing  
APPLICANT: Gibson, Bradford W.

```

Db      697  LRVFSFSPARSLRLITAFASLSVETLSLNLESDATWQJDLHFPFGLSFRKVEMLKPHSQ 756
Qy      841  I PVSCEELPERSRRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSGDSVEIHLANTC 900
Db      757  I PVSCEELPERSRRLSLRSLSCNVSSPIFKAGHSVALQMMFNTLVNNSGDSVEIHLANTC 816
Qy      901  NNEBSDLLEDSNATTTIPIILYPINILIODQEDSTLYVSTFKPKIHOVKMYQVRIOPS 960
Db      817  NNEBSDLLEDSNATTTIPIILYPINILIODQEDSTLYVSTFKPKIHOVKMYQVRIOPS 876
Qy      961  IHDNIPFLKAVGVGPQPSGPIITHQMSVQMEPPVPCHYEDLERLPAAEPCIPGALFR 1020
Db      877  IHDNIPFLKAVGVGPQPSGPIITHQMSVQMEPPVPCHYEDLERLPAAEPCIPGALFR 936
Qy      1021  CPVVPORLIVQVIGTELVEITEASSMPSLCSLSLISFNSSKPHHLXGNSASLAQVVMK 1080
Db      937  CPVVPORLIVQVIGTELVEITEASSMPSLCSLSLISFNSSKPHHLXGNSASLAQVVMK 996
Qy      1081  VDVPYERQMLLYLVLSGIGLILLIPIVLKYVGFGRNLKEKMEAGRGVPGNIPADS 1140
Db      997  VDVPYERQMLLYLVLSGIGLILLIPIVLKYVGFGRNLKEKMEAGRGVPGNIPADS 1056
Qy      1141  EQLASGOEAGDPGCIKPIHEKDSGSGGKD 1170
Db      1057  EQLASGOEAGDPGCIKPIHEKDSGSGGKD 1086

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## RESULT 12

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PCT-US05-02350-80
; Sequence 80, Application PC/TUS0502350
; GENERAL INFORMATION:
; APPLICANT: Avalon-Soffer, Michal
; APPLICANT: Levine, Zurit
; APPLICANT: Sella-Tavor, Osnat
; APPLICANT: Diber, Alex
; APPLICANT: Shemesh, Ronen
; APPLICANT: Toporik, Amir
; APPLICANT: Rotman, Galit
; APPLICANT: Nemzer, Sergey
; APPLICANT: Rosenberg, Avi
; APPLICANT: Dahanay, Dvir
; APPLICANT: Wool, Assaf
; APPLICANT: Cojocaru, Gad S.
; APPLICANT: Akiva, Pinchas
; APPLICANT: Pollock, Sarah
; APPLICANT: Savitsky, Kimeret
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING
; FILE REFERENCE: 28487
; CURRENT APPLICATION NUMBER: PCT/US05/02350
; NUMBER OF SEQ ID NOS: 1155
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-02350-80

```

```

Query Match      63.6%; Score 3885; DB 1; Length 750;
Best Local Similarity 99.5%; Pred. No. 5.6e-287;
Matches 745; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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```

Qy      1  MKDCITVMAMALLSGFFFAPASSYMLDVAGARSFSPARRHFGYRVLVQNGVTVGA 60
Db      1  MKDCITVMAMALLSGFFFAPASSYMLDVAGARSFSPARRHFGYRVLVQNGVTVGA 60
Qy      61  PGEENSGSLYQCCSGGCHCLPYTLRGSNYSKYLQMTLADPTDGSGLIADCPGLSTRCD 120
Db      61  PGEENSGSLYQCCSGGCHCLPYTLRGSNYSKYLQMTLADPTDGSGLIADCPGLSTRCD 120

```

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Qy      121  QNTYLSGLCYLFRONTQGPMLQGRPGFOECIKGNVDLVFLPDSMSLQDPEFOKILDFMK 180
Db      121  QNTYLSGLCYLFRONTQGPMLQGRPGFOECIKGNVDLVFLPDSMSLQDPEFOKILDFMK 180
Qy      181  DVMKLSNTSYQPAVQFSTSYTERPDSYVYRKQDPAALLKIVKMLLTNTFGAINV 240
Db      181  DVMKLSNTSYQPAVQFSTSYTERPDSYVYRKQDPAALLKIVKMLLTNTFGAINV 240
Qy      241  ATEVFRBELGARPRATVLLIITDGEATDSGNIDAAODIIRYIIIGIKHPQTERSOETLH 300
Db      241  ATEVFRBELGARPRATVLLIITDGEATDSGNIDAAODIIRYIIIGIKHPQTERSOETLH 300
Qy      301  KFASKPASEFVKILDTPEKLDLFTBELOKKIYIIEGTSKODLTSFNNELSSGSIADLSR 360
Db      301  KFASKPASEFVKILDTPEKLDLFTBELOKKIYIIEGTSKODLTSFNNELSSGSIADLSR 360
Qy      361  GHAVGAVGAKDMAAGFLDLKADLQDDTFI GNEPLTPEVAGYLYGVVTLPSRQKTSLL 420
Db      361  GHAVGAVGAKDMAAGFLDLKADLQDDTFI GNEPLTPEVAGYLYGVVTLPSRQKTSLL 420
Qy      421  ASGAPRYQHMGRVLLTPOEPQGGHMSOVOTIHGTQIGSYRFGHLCGVVDVQDDETELLI 480
Db      421  ASGAPRYQHMGRVLLTPOEPQGGHMSOVOTIHGTQIGSYRFGHLCGVVDVQDDETELLI 480
Qy      481  GAPLFYGEORQGRVFIYQRRQLGFEVSELOQDPGYPLGRFGAITLTDINGDLVDA 540
Db      481  GAPLFYGEORQGRVFIYQRRQLGFEVSELOQDPGYPLGRFGAITLTDINGDLVDA 540
Qy      541  VGAPLEQGAIVYIFNGRHGSLSPQPSORITGTVLSGIQWFGRSIHGVKDLBEDGLADVA 600
Db      541  VGAPLEQGAIVYIFNGRHGSLSPQPSORITGTVLSGIQWFGRSIHGVKDLBEDGLADVA 600
Qy      601  VGASQMTVLSRPPVDMVTMLSPSPAEIPVHVECSYSTSNMKSGVNTTICFOIKSLY 660
Db      601  VGASQMTVLSRPPVDMVTMLSPSPAEIPVHVECSYSTSNMKSGVNTTICFOIKSLY 660
Qy      661  POFQGRVLANLYTLQDGHRTRRRGLFPGRHELRNLIATVTSMSCTDPSFFPVCVOD 720
Db      661  POFQGRVLANLYTLQDGHRTRRRGLFPGRHELRNLIATVTSMSCTDPSFFPVCVOD 720
Qy      721  LISFINVSLNFSLWEEEGTIPRDOQAQKD 749
Db      721  LISFINVSLNFSLWEEEGTIPRDOQAQKD 749

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## RESULT 13

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US-11-043-770-80
; Sequence 80, Application US/11043770
; GENERAL INFORMATION:
; APPLICANT: Avalon-Soffer, Michal
; APPLICANT: Levine, Zurit
; APPLICANT: Sella-Tavor, Osnat
; APPLICANT: Diber, Alex
; APPLICANT: Shemesh, Ronen
; APPLICANT: Toporik, Amir
; APPLICANT: Rotman, Galit
; APPLICANT: Nemzer, Sergey
; APPLICANT: Rosenberg, Avi
; APPLICANT: Dahanay, Dvir
; APPLICANT: Wool, Assaf
; APPLICANT: Cojocaru, Gad S.
; APPLICANT: Akiva, Pinchas
; APPLICANT: Pollock, Sarah
; APPLICANT: Savitsky, Kimeret
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING
; FILE REFERENCE: 28488
; CURRENT APPLICATION NUMBER: US/11/043,770
; NUMBER OF SEQ ID NOS: 1155
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80

```

LENGTH: 750  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-043-770-80

Query Match 63.6%; Score 3885; DB 7; Length 750;  
Best Local Similarity 99.5%; Pred. No. 5.6e-287;  
Matches 745; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 MKDSCITMAMALLSGFFFPAPASSYNDVGRARSFSPRRGRHGYVLOVGNVYGA 60
DB 1 MKDSCITMAMALLSGFFFPAPASSYNDVGRARSFSPRRGRHGYVLOVGNVYGA 60
QY 61 PGEBSSTSLVQCCSGTGHCPLVTLRGSNTSKYLGMTLADPDGSLIACDPGSRCD 120
DB 61 PGEBSSTSLVQCCSGTGHCPLVTLRGSNTSKYLGMTLADPDGSLIACDPGSRCD 120
QY 121 QNTYLSGLCYLFRNLQGPMLQGRPGFECIKANVDVFLFDGSMSLQDFEOKILDPMK 180
DB 121 QNTYLSGLCYLFRNLQGPMLQGRPGFECIKANVDVFLFDGSMSLQDFEOKILDPMK 180
QY 181 DVMKLSNTSYQFAAVQSTSYKTEFSDYVKRDPALLKHVGMILLNTFGALINYV 240
DB 181 DVMKLSNTSYQFAAVQSTSYKTEFSDYVKRDPALLKHVGMILLNTFGALINYV 240
QY 241 ATEVPREELGARPDATKYLIIITDGBATDSGNIDAKDIIIRYIIGIGHFQTKESQETLH 300
DB 241 ATEVPREELGARPDATKYLIIITDGBATDSGNIDAKDIIIRYIIGIGHFQTKESQETLH 300
QY 301 KEASPKASEFVKILDTFEKLDLFTLEOKIYVLEGTSKODLTSFNMELSSSGISADLSR 360
DB 301 KEASPKASEFVKILDTFEKLDLFTLEOKIYVLEGTSKODLTSFNMELSSSGISADLSR 360
QY 361 GHAVGAVGAKDMAGGFLDLKADLDDDTFIGNBPLTEVRAGYLGTYTWMPSRQKTSLL 420
DB 361 GHAVGAVGAKDMAGGFLDLKADLDDDTFIGNBPLTEVRAGYLGTYTWMPSRQKTSLL 420
QY 421 ASQAPRYHMGVYLLFQEPQGGHWSQVQTHGTQISYFGGELCGVDVDDGTELLLI 480
DB 421 ASQAPRYHMGVYLLFQEPQGGHWSQVQTHGTQISYFGGELCGVDVDDGTELLLI 480
QY 481 GAFPLFYGORGRVFTYORROLGFESEVSELQDPPYPLGRFGEAITALTIDINGDLVDA 540
DB 481 GAFPLFYGORGRVFTYORROLGFESEVSELQDPPYPLGRFGEAITALTIDINGDLVDA 540
QY 541 VGAPLEEGGAVYIFNGRHGGLSPQSPQRIEGTVLSGIQWFGRSIHGVXDLBGDLADVA 600
DB 541 VGAPLEEGGAVYIFNGRHGGLSPQSPQRIEGTVLSGIQWFGRSIHGVXDLBGDLADVA 600
QY 601 VGABEQMIVLSRPVYDVTILMSFPAIPVHEVECSYSTSNKMEGVNITICFOIKSLY 660
DB 601 VGABEQMIVLSRPVYDVTILMSFPAIPVHEVECSYSTSNKMEGVNITICFOIKSLY 660
QY 661 POFQRLVANTLYTLQDLGHRTRRGLPGRHLELRNIAVTTSMSCDPSFHPVVCOD 720
DB 661 POFQRLVANTLYTLQDLGHRTRRGLPGRHLELRNIAVTTSMSCDPSFHPVVCOD 720
QY 721 LISPIVSLNLSLWEEBETPRDQAGKD 749
DB 721 LISPIVSLNLSLWEEBETPRDQAGKD 749
```

RESULT 14  
US-11-062-290-2  
Sequence 2, Application US/11062290  
GENERAL INFORMATION:  
APPLICANT: KAPUSTAY, PAMELA M.  
TITLE OF INVENTION: LFA-1 ALPHA SUBUNIT ANTIBODIES AND METHODS OF USE  
FILE REFERENCE: 046007/0272304  
CURRENT APPLICATION NUMBER: US/11/062,290  
CURRENT FILING DATE: 2005-02-17  
PRIOR APPLICATION NUMBER: US/10/261,164

PRIOR FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 589  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-062-290-2

Query Match 50.2%; Score 3066; DB 7; Length 589;  
Best Local Similarity 99.8%; Pred. No. 9.6e-225;  
Matches 588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 26 YNLVGRARSPRRARHGYRVLQVGNVYVGAPEBGNSTSLVQCCSGTGHCPLVTL 85
DB 1 YNLVGRARSPRRARHGYRVLQVGNVYVGAPEBGNSTSLVQCCSGTGHCPLVTL 85
QY 86 RGSNTSKYLGMTLADPDGSLIACDPGSRCDQNTYLSGLCYLFRNLQGPMLQGRP 145
DB 86 RGSNTSKYLGMTLADPDGSLIACDPGSRCDQNTYLSGLCYLFRNLQGPMLQGRP 145
QY 146 GFQECIKANVDVFLFDGSMSLQDFEOKILDPMKDVKKLSNTSYQFAAVQSTSYKTE 205
DB 146 GFQECIKANVDVFLFDGSMSLQDFEOKILDPMKDVKKLSNTSYQFAAVQSTSYKTE 205
QY 206 FDESDYVKRDPALLKHVGMILLNTFGALINYVATEVPREELGARPDATKYLIIITDG 265
DB 206 FDESDYVKRDPALLKHVGMILLNTFGALINYVATEVPREELGARPDATKYLIIITDG 265
QY 266 EATDSGNIDAKDIIIRYIIGIGHFQTKESQETLHKEASPKASEFVKILDTFEKLDLFT 325
DB 266 EATDSGNIDAKDIIIRYIIGIGHFQTKESQETLHKEASPKASEFVKILDTFEKLDLFT 325
QY 326 ELQKIVIGESTSKODLTSFNMELSSSGISADLSRGAHVAVGAKDMAGGFLDLKADLQ 385
DB 326 ELQKIVIGESTSKODLTSFNMELSSSGISADLSRGAHVAVGAKDMAGGFLDLKADLQ 385
QY 386 DDTFIGNBPLTEVRAGYLGTYTWMPSRQKTSILASGARRYOMGVYLLFQEPQGGHWS 445
DB 386 DDTFIGNBPLTEVRAGYLGTYTWMPSRQKTSILASGARRYOMGVYLLFQEPQGGHWS 445
QY 446 SOVQTHGTQISYFGGELCGVDVDDGTELLLIQAPLFGSEORGRVFTYORROLGFE 505
DB 446 SOVQTHGTQISYFGGELCGVDVDDGTELLLIQAPLFGSEORGRVFTYORROLGFE 505
QY 506 EVSELQDPPYPLGRFGEAITALTIDINGDLVDAVAGAPLEEGGAVYIFNGRHGGLSPQ 565
DB 506 EVSELQDPPYPLGRFGEAITALTIDINGDLVDAVAGAPLEEGGAVYIFNGRHGGLSPQ 565
QY 566 SQRLEGTVLSGIQWFGRSIHGVXDLBGDLADVAVGABEQMIVLSRSP 614
DB 566 SQRLEGTVLSGIQWFGRSIHGVXDLBGDLADVAVGABEQMIVLSRSP 614
```

RESULT 15  
US-60-651-235-76  
Sequence 76, Application US/60651235  
GENERAL INFORMATION:  
APPLICANT: JOSELOFF, Elizabeth et al.  
TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF  
FILE REFERENCE: C0001581  
CURRENT APPLICATION NUMBER: US/60/651,235  
NUMBER OF SEQ ID NOS: 3512  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 76  
LENGTH: 1153  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-60-651-235-76  
Query Match 25.6%; Score 1564; DB 8; Length 1153;  
Best Local Similarity 34.3%; Pred. No. 7e-110;

Matches 409; Conservative 212; Mismatches 464; Indels 108; Gaps 38;

```

Qy 6 ITWAMALLSGFFPAPASYNLDVRCARSPSPRAGHFGRYLV- GNCVYIGABE- 63
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 6 LLLALALTCHEF-----NLDENAMTQ--ENARGFGOSVQGLGSSVVGAPDEI 54
Qy 64 --GNSGSLVYCCGSGTGCHLPVTLR-GSNYTSKYLGMATDPDGSILACDPGLSRCD 120
Dy 55 VAAHQSGSLVYCCDYSTGSCERIRLQVPEAVNMISLGLAATSPQGLAGPVTWQCS 114
Qy 121 QNTILSGICLYFRQNLQCPMLQGRPGFQECIKG---NVDLVFLFDGMSIQDPBQKIL 176
Dy 115 ENTIVYKGLCFPGSNLR---QQPQKPEALRGCPQEDSDIAFLDGSGLIPHDFFRMK 170
Qy 177 DEMKQVMKLSNTSYQFAAYOESTSYKTEPFDSDYVKRKPDPALLKHVKHMLLJNTEGA 236
Dy 171 EFVSTVMEQLKSKSLTBSLMQYSEBFRHFTFKFQNNPNRSLVKPITQLGRHTATYG 230
Qy 237 INVYATEVEFRELGARPDATKVLIIITDGE--ATDSGNIDAKD-----IRYIIIGIKH 289
Dy 231 IRKYVRELFININGARKNAFKILVITDGEKFGDPLGYEDVYIPEADREGVIRYIVGVDA 290
Qy 290 FQTEESQETLHKPKASKPASEFVKILDTPEKLDLTELQKTIYVEGTSKODLTSFMMEL 349
Dy 291 FRSEKSRQELNNTIASKPPRDHVFQVNNFEALKTIIQNLREKIFALBGTQTSSSSFHEM 350
Qy 350 SSS$ISADLSRGHAVVAGAKDWAGFLDKADLQDDTFIGNEBLTPREVAGYLYVT 409
Dy 351 SQBFSAITNGSLPSTVSGSYDNAGVYF-LYTSKSKSTFIMTRVDSMDNDATILGYAAA 409
Qy 410 WLPFRQKTSLLASGAPRYQHMGRVLLFQEPQGGHMSQVOTIHGTQISYFGELCGVDV 469
Dy 410 -IIRNRVQSLVLAGAPRYQHIGLVAMFR--QNTGMMESNANVKGTOIGAYFGASLCSVDV 466
Qy 470 DQDGETELLIGAPLIFYGORGGRVYIY----QRQUGFEVESELQDPGYPLGRGEA 524
Dy 467 DSNSTDLVLIGAPHYEQTRGQVSVCLPRGQARWQCDAY--LYGEOQPGWRFGAA 524
Qy 525 ITALTIDINGDLVAVAGAPLEB--QGAVYIIFNGRHG-GLSPQSPORIEGTQVLSGIOWF 581
Dy 525 LTVAGDVAGDCLTVATIGAPBEBDNKRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYF 584
Qy 582 GRSIHGVKDLBEGDLADVAGAESQMTIVLSRPVVDVTLMSFSPABLPVHEVECSYSTS 641
Dy 585 GQSLSGQDGLMDGLVLDLTGAGQHVLLRSQPVLRVKAIMEFNPBEVARNVFECDQVY 644
Qy 642 NKMTKEGVNITTCFOI-KSLYPOF-QGRLVANLYTTLQLDGHRTRRGLFPGGRHRLRNT 699
Dy 645 -KGEAGEVRVCLHVQKSTRDLRLEGQIQSVVYTDLALDSGRPHSRVAFNETKNSTRQT 703
Qy 700 AVT-TSNMCTDPSFHPVQODLISPINVSINFSLMEBEGTPRDQAGKDIPLLRPSL 758
Dy 704 QVLELTQTCETLKIQLPNCIEDPPVSPYVLRNLSL--VGTPLS--AFGN-----LRPVL 753
Qy 759 HSEFWEL-----PEKQCGEDKCEANLRVSPARSRLRLTAASLVELSLNLEED 813
Dy 754 AEDAQRLEFALFPEKQCGANDNICODDLSTFSFMSLDCLVVGGBRENFVTVYVRNGED 813
Qy 814 AYWQOLHLPFPGSLFRVEML---KHSQIPVSCBEL--PEESRLSRALSCNVSSPIF 868
Dy 814 SYRQVTEFFPLDLSYRKVSTLQNRQSRWRLACESASSTEVSGVL-KSTSCSINHPIF 872
Qy 869 KAGSHVALQMMFNTLVNNSMGDSVELHANVTCNNEDSDLEDNSATYI--IPILYPINI 925
Dy 873 PENSEVTNITFDVDSKASLQNKLLKANKVTSENN---MPTNKTEFOLELPVKIAYYM 928
Qy 926 LIQDQEDSTLYVSTPKGPKIHQVKMYQVRIQPSIHDNIPITLEAVVGVQPPSEEGPIT 985
Dy 929 VVTSHGASTKTLNFTASENTSRVMQHQYV---SNLQGRSLP-ISLVFLVVRNLNQYIWM 984
Qy 986 HQNVQMEPPY--FCHYEDLERLPDAEPCLPGALFRCFVY-----F 1025
Dy 985 DRPVTSENLSTCHTK--ERLPSHSD--FLAELRKAPVNVCSIAVCORIQCDIPFPGI 1040

```

```

Qy 1026 ROEILVQVIGTLELVEIBAS-SMFSLSSSLISFNSSKRHFLYGSNAPL-AQVVMKVYV 1083
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 1041 QEBFNATLKGNLSFDWYIKTSHHHLIVSTAELLFNDVSFTLLPGQAFVRSQTEYTER 1100
Qy 1084 VYERQMLYLYVLSGIGGLLLLLIFVLYVYGFPPKRLKERMAGRGVNPNGIP 1136
Dy 1101 FEVVPNPLPLIVGSSVGGLLLLALITALVYKLGFPKQYKDMSEBG--GPPGAPR 1152

```

Search completed: August 29, 2005, 19:37:09  
 Job time : 92 secs